



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 96343

TO: Sarvamangala Devi
Location: cm1/7e15/7e12
Art Unit: 1645
Friday, June 20, 2003
Case Serial Number: 715876

From: Paul Schulwitz
Location: Biotech-Chem Library
CM1-6B06
Phone: 305-1954

paul.schulwitz@uspto.gov

Search Notes

STIC-Biotech/ChemLib

96343

From: STIC-ILL
Sent: Wednesday, June 11, 2003 9:57 AM
To: STIC-Biotech/ChemLib
Subject: FW: 09/715,876

RECEIVED

JUN 11 2003

(STIC)

-----Original Message-----

From: Devi, Sarvamangala
Sent: Wednesday, June 11, 2003 9:54 AM
To: STIC-ILL
Subject: 09/715,876

Beverly:

Would you please perform a sequence and an interference search for SEQ ID NO: 7 and SEQ ID NO: 8 in application SN 09/715,876?

Thank you.

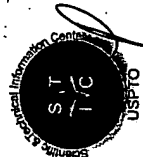
S. DEVI, Ph.D.
AU 1645
CM1-7E15
Mailbox: CM1-7E12

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 6/11
Date Completed: 6/20
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____

SEARCH REQUEST FORM



STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 112253

To: Sarvamangala Devi
Location: CM17E157E12
Art Unit: 1645
Tuesday, January 20, 2004

Case Serial Number: 09/715876

From: Beverly Shears
Location: Remsen Bldg.
RM 1A54
Phone: 571-272-2528
beverly.shears@uspto.gov

Shears, Beverly

112253

From: Devi, Sarvamangala
Sent: Thursday, January 15, 2004 3:05 PM
To: Shears, Beverly
Subject: 09/715,876

Beverly:

Please perform a sequence and an interference search for an N-terminal nucleic acid sequence comprising nucleotides 52 to 1296 of SEQ ID No.7 in application SN 09/715,876.

Thank.

S. DEVI, Ph.D.
AU 1645

STAFF USE ONLY

Date completed: 01-14-04
Searcher: Beverly e 2528
Terminal time: 23
Elapsed time: _____
CPU time: _____
Total time: 23
Number of Searches: _____
Number of Databases: _____

Search Site: STIC
CM-1
Pre-S
Type of Search: N.A. Sequence
A.A. Sequence
Structure
Bibliographic
Vendors: IG
STN
Dialog
APS
Geninfo
SDC
DARC/Questel
Other ()

Db	772	TC	TTT	GGT	AT	CT	CT	AT	CA	CA	TAT	CA	AA	AT	GT	TC	CG	GT	TAT	CG	TCA	T	TAT	TG	AC	831				
Qy	781	GC	TTA	TAT	TT	CT	GT	CA	GAG	TG	TAA	CC	AA	TAT	ACT	T	T	AG	CA	TAT	CA	CA	AT	GA	T	TACT	840			
Db	832	GC	TTA	TAT	TT	CT	CT	CA	GA	TAA	CC	AG	TAT	CA	AT	TG	T	CG	TAT	AA	AA	AT	GA	T	TACT	891				
Qy	841	TG	TG	CT	GG	CA	GT	CG	TG	TG	CA	AA	GT	TAA	AC	TT	T	CA	CT	T	T	AA	GA	CT	GA	TACA	900			
Db	892	TG	TG	TT	GAT	GAT	TAT	TG	GC	CA	AT	CG	TCA	CC	TT	T	CA	CT	T	T	AA	AT	GG	CA	CT	GAT	TAA	951		
Qy	901	AG	TG	AT	CC	CG	AT	CT	TA	AC	GG	TAT	TG	T	CA	T	TG	T	CT	CA	AC	T	GA	AA	CAG	TTAC	960			
Db	952	AG	TG	AT	CC	CG	AT	CT	TA	AC	GG	TAT	TG	T	CA	T	TG	T	CT	CA	AC	T	GA	AA	CAG	TTAC	1011			
Qy	961	AC	CA	CT	GT	CT	CA	TACT	TTA	AC	CA	TT	CA	AT	CC	AA	GT	TG	T	GA	T	AA	AA	CA	AA	CA	AT	CG	1020	
Db	1012	AC	CA	CT	GT	CT	CA	TACT	TTA	AC	CA	TT	CA	AT	CC	AA	GT	TG	T	GA	T	AA	AA	CA	AA	CA	AT	CG	1071	
Qy	1021	AT	TT	TG	CA	AC	CT	TAT	T	CC	AA	CG	CA	TAC	CA	AT	CA	CA	CT	T	CAT	AT	TG	TG	TG	TG	CA	CT	1080	
Db	1072	AT	TT	TG	CA	AC	CT	TAT	T	CC	AA	CG	CA	TAC	CA	AT	CA	CA	CT	T	CAT	AT	TG	TG	TG	TG	CA	CT	1131	
Qy	1081	TAT	CT	GA	CT	AA	GA	CT	CG	CA	CA	AT	TG	TG	TG	TG	AA	CA	GA	CT	ACT	CT	TAT	TG	TG	TG	TG	CC	AT	1140
Db	1132	TAT	CT	GA	CT	AA	GA	CT	CG	CA	CA	AT	TG	TG	TG	TG	AA	CA	GA	CT	ACT	CT	TAT	TG	TG	TG	TG	CC	AT	1191
Qy	1141	CAT	ACT	AC	CA	CA	CT	GT	T	TAC	CA	GT	GA	TG	CA	AG	GA	CA	AT	CA	CT	ACT	CA	CC	CA	CA	CT	CG	1200	
Db	1192	CAT	ACT	AC	CA	CA	CT	GT	T	TAC	CA	GT	GA	TG	CA	AG	GA	CA	AT	CA	CT	ACT	CA	CC	CA	CA	CT	CG	1251	
Qy	1201	AC	CA	AT	CC	AA	CT	GA	T	TCA	AT	TG	CA	CA	AG	TG	GG	TG	T	CA	AG	T	TCA	1245						
Db	1252	AC	CA	AT	CC	AA	CT	GA	T	TCA	AT	TG	CA	CA	AG	TG	GG	TG	T	CA	AG	T	TCA	1296						

RESULT 3

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US-10-245-802-21
;
; RESULT: 3
;
; US-10-245-802-21
; Sequence 21, Application US/10245802
; Publication No. US20030124134A1
;
; GENERAL INFORMATION:
;
; APPLICANT: Edwards, John E.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS TO VACCINATE AGAINST
; TITLE OF INVENTION: DISSEMINATED CANDIDIASIS
; FILE REFERENCE: 013361.4003
;
; CURRENT APPLICATION NUMBER: US/10/245,802
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 09/715,876
; PRIOR FILING DATE: 2000-11-18
;
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
;
; LENGTH: 4383
;
; TYPE: DNA
;
; ORGANISM: Candida albicans
;
; US-10-245-802-21

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Qy	181	ACTACTTCCAAACATCTGTGTGATTTAACTGCGGATGGTGTAAATATGCTACTTGTCAA	240
Db	928	ACTACTTCTCAAAACATCTGTGTGATTTGACTGTCTCACTGGTGTAAATATGCTCATGTCAA	987
Qy	241	TTTTTATCTGGTGAAGAAATTCACACTTTTCTTACATTAACATGTACTGTGAACGAGCT	300
Db	988	TTTCAGGCGAGGTGAAGATTTATGACCTTTTCTACATTAACATGTACTGTGAACCAATACT	1047
Qy	301	TTGAAATCATCCATTAAGGCATTTGGTACAGTTTACTTTTACC AATTTGCATTTCAATGTGGT	360
Db	1048	TTGACTCCATCTANTTAAGGCTTTGGGTACTGTCACTTACCACCTTCAATGTAGGT	1107
Qy	361	GGNACAGGTTTCATCAACTGATTTGGAGAGATTTCTAAATGTTTACTCTGCTGGTACCAATACA	420
Db	1108	GGAACTGGTGTCTTCTGTTGATTTGGAGAGATTTCTAAATGTTTACTCTGCTGGTACTAACACA	1167
Qy	421	GTCACATTTAATGATGGTGATAAAGATATCTCAATTTGATTTGAGTTTGGAAAGTCAACC	480
Db	1168	GTTCATTTAATGATGGTGGCAAGAAATCTCTATTAAATTTGATTTTGAAGGTCAAT	1227
Qy	481	GTTGATCCAAGTGCAATATTTGTATGCTTCCAGAGTTATGCCAAGTCTCAATTAAGGTCA	540
Db	1228	GTGATGCCAAAAGGGTACTTAATGATTTCCAGAGTTATACC AAGTCTCAACAAAGTCTCA	1287
Qy	541	ACTCTTTTGTGGCACCAACATGTGAAAATGGTTACACATCTGGTACAAATGGGTTCTCC	600
Db	1288	ACTCTTTTGTGGCACCAACATGTGCAATGGTTACACATCTGGTACAAATGGGATTCGGT	1347
Qy	601	AGTAGTAACGGTGACGTTGCTATTGATTTGCTCAAAATTTTCAATATTTGGTATCAACAAAGGA	660
Db	1348	AACACTTATGGTGATGTTCAAAATTTGACTGTTCAAAATATTCAATTTGTTATTTACAAAGGA	1407
Qy	661	TTAAATGATTTGGAATTTATCCGGTTTTCATCTGGAATCAATTTAGTTACATTAACACTTGTACA	720
Db	1408	TTGAATGATTTGGAATTTATCCGGTTTTCATCTGGAATCAATTTAGTTACATTAACACTTGTACA	1467
Qy	721	TCTAATGGGAATTCAGATTAATATCAAAATGTACCTGCTGGTATTGCTGCATTTATTTGAT	780
Db	1468	TCTAATGGGTATCTTTATCACATATAAAATGTTCTCTGCCGTTATGCTCCATTTGTTGAC	1527
Qy	781	GCTTATATTTCTGCTACAGATGTTTAAACCAATATATCTTTAGCAATATACCAATGATTTACT	840
Db	1528	GCTTATATTTCTGCTACAGATGTTTAACTCGTACACCTTGTGCTATGCTTAATGAATATACT	1587
Qy	841	TGTGCTGGCAGTCTGCTGCAAAAGTAAACCTTTTCACTTTAAGATGGACTGGATCAAGAAT	900
Db	1588	TGTGCTGGGTGTTATGGCAACGTGCACCTTTTCAATTAAGATGCACTGGATACAGAAAT	1647
Qy	901	AGTGATGCCGAGTCTAAACGGTATTGTCTATTTGTGTCTACAATAGAACAGTTTACAGACGT	960
Db	1648	AGTGATGCTGGATCTAAACGGTATTGTCTATTTGTGGTCTACTACCAGAACAGTTTACAGACGT	1707
Qy	961	ACCACGTCTGCTACTACTTTTACATTTCAATCCAAGTGTGTGATATAAACCAAAACAATCGAA	1020
Db	1708	ACTACGGCGTGACCACTTACATTTGATCTCTAACCGGCAACAAACTTAAGCAATTTGAA	1767
Qy	1021	ATTTTGCACCTTATTTCCAAACCACTACCAATCACAACTTCATATTTGGTGTGCTACTTCC	1080
Db	1768	ATTTTGGAAACCTTATTTCCAAACCACTACAATCACAACTATATTTGGTGTGCTACTTCC	1827
Qy	1081	TATCTGACTTAAGACTGCAACCAATTTGGTGGAAACAGCTACTGTTATTTGTTGATGTGCATAT	1140
Db	1828	TACCTGACCAAAACTGCAACCAATTTGGGGAACCTGCTACTGTTATTTGTTGATATTCATAT	1887
Qy	1141	CATACTACCACAACTGTTTACCAGTGAATGGACAGGAAACAATCACTACCAACCAACTCGT	1200
Db	1888	CACACTACCACTACTGTTTACCAGTAAATGGACAGGAAACAATTTACTTCCACCAACACAT	1947
Qy	1201	ACCAATCCAACTGATTTCAATTTGACACAGTGGTGTACAAAGTTCCA	1245
Db	1948	ACTAATCCAACTGATTTCAATTTGACACAGTGGTGTACAAAGTTCCA	1992

RESULT 4					
US-10-245-802-11					
; Sequence 11, Application US/10245802					
; Publication No. US20030124134A1					
; GENERAL INFORMATION:					
; APPLICANT: Edwards, John E.					
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS TO VACCINATE AGES					
; FILE REFERENCE: 013361.4003					
; CURRENT APPLICATION NUMBER: US/10/245,802					
; CURRENT FILING DATE: 2002-09-13					
; PRIOR APPLICATION NUMBER: US 09/715,876					
; PRIOR FILING DATE: 2000-11-18					
; NUMBER OF SEQ ID NOS: 24					
; SOFTWARE: PatentIn version 3.2					
; SEQ ID NO 11					
; LENGTH: 3360					
; TYPE: DNA					
; ORGANISM: Candida albicans					
US-10-245-802-11					
Query Match 76.1%; Score 947.4; DB 15; Length 3360;					
Best Local Similarity 85.1%; Pred. N. 2.7e-203;					
Matches 1059; Conservative 0; Mismatches 186; Indels 0; Gaps 0					
Qy	1	AAGACAATC	ACCTGGTGTGTTTGATAGTTTTTAATTCAATTAACTTGGTCGAATGCTGCTACT	60	
Dd	52	AAGACAATC	ACCTGGTGTGTTTCAACACAGTTTTTAATTCAATTGACCTTGGTCTGAATGCTGCTACT	111	
Qy	61	TATGCTTTCAA	AGGCCACAGGATACCCAACTTGGAAATGCTGTTTTGGGTTGGTCTTAGAT	120	
Dd	112	TATAATTAT	TAAGGNACAGAACCCCACTTGGAAATGCTGTTTTGGGTTGGTCTTAGAT	171	
Qy	121	GGTACCACTG	CCAATCCAGGGGATACATTCACATTTGAATATGCCCATGTGTGTTTAAATAT	180	
Dd	172	GGTACTAGTC	GAAGTCCGGGAGATACATTCACATTTGAATATGCCCATGTGTGTTTAAATAT	231	
Qy	181	ACTACTTCACA	AAACATCTGTTGATTTTAATCTGCCGATGGTGTTPAAATATGCTACTTGTGCA	240	
Dd	232	ACTACTTCTC	AAAACATCTGTTGATTTGATGCTCTCAITGGTGTTPAAATATGCTACTGCA	291	
Qy	241	TTTTTATCTCG	TGAAGAATTCACAACTTTTCTACATTAACATGTACTGTGAACGACGCT	300	
Dd	292	TTTCAGGCAGG	TGAAGATTTATGACCTTTTCTACATTAACATGTACTGTGAGCAATACT	351	
Qy	301	TTGAAATCAT	CATTAAGGCATTTGGTACAGTTACTTACCAATTCATTCATGTTGGT	360	
Dd	352	TTGACTCCAT	CTATTAAAGCTTTGGGTACTGTCACTTACCACCTTGCAATTCATGTAGT	411	
Qy	361	GGACAGGTTCA	TCACTCAATTTGCAAGATTTCTAAATGTTTTTACTGCTGGTACCAATACA	420	
Dd	412	GGAACTGGTTC	TCTCTGTTGATTTGGAAGATTTCTAAATGTTTTTACTGCTGGTACTAACACA	471	
Qy	421	GTCAATTTAAT	GATGGTGTGATAAGATATCTCAAATTGATTTGAGTTTGAAAGTCAACC	480	
Dd	472	GTATCAATTTA	TATGATGGTGGCAAGAAATCTCTATTAAITGTTGTTTGAAGGTCAAAAT	531	
Qy	481	GTTGATCCAAG	TGCATATTTGTATGCTTCCAGATTTAGCCAAAGTCTCAATTAAGGTCAACA	540	
Dd	532	GTGATCCAAA	AGGGGTACTTTAACTGATTTCCAGAGTTTATACCAAGTCTCAACAAAGGTCA	591	
Qy	541	ACTCTTTTTTG	TGGCACCAACAATGTCAAAATGGTTACACATCTGGTACAAATGGGTTCTCC	600	
Dd	592	ACTCTTTTTTG	TGGCACCAACAATGTGAAATGGTTACACATCTGGTACAAATGGGTTCTCGT	651	
Qy	601	AGTAGTAACGG	TGAAGTTGCTATTGATTTGCTCAAAATATTCAATTTGGTATCAAAAAAGA	660	
Dd	652	AACACTTATG	TGTGATTTCAAATTCAGTGTCAAATATTTCAATTTGGTATTACAAAAAGA	711	
Qy	661	TTAAATGATG	TGAAATATCCCGTTTTCATCTGAATCATTTAGTATCACTTAAACTTGTACA	720	
Dd	712	TTGAATGATG	TGAAATATCCCGTTTTCATCTGAATCATTTAGTATCACTTAAACTTGTACA	771	

187 TCACAAACATCTGTTGATTTAACTCCGATGGTGTAAATATGCTACTCTCAATTTAT 246
238 GATCAAAACATCTGTTGATTTAACTCCGATGGTGTAAATATGCTACTCTCAATTTAT 297
247 TCTGGTGAAGAAATTCACAACTTTTCTACATTAACATGATCTGTGAACGAGCTTTGAAA 306
298 TCAGGTGAAGAAATTCACAACTTTTCTACATTAACATGATCTGTGAACGAGCTTTGAAA 357
307 TCATCCATTAAGCAATTTGTTGATGATCTTTTACCAATTCATTTCAATTTGTTGGGAACA 366
358 TCATCTATTAAAGCTTTGGGTACGGTTACTTTTACCAATTTCAATTTAATGTTGGTGAACA 417
367 GGTTCATCACTGATTTGGAAGATTTCTAAATGTTTACTCTGCTGATCAATGATGATCA 426
418 GGTTCATCGGTTGATTTGGAAGTTCTCAATGTTTAAAGCTGGCACCAACACAGTTACT 477
427 TTTAATGATGCTGATTAAGATATCTCAATTTGATTTGAGTTTCAAAAGTCAACCGTTGAT 486
478 TTTAATGATGCTGATTAAGAAATTTCTCAATTTGATTTGAGTTTGAAGAAACAAACGAGAT 537
487 CCAAGTGCATTTATGTTGATGCTTCCAGATTTATGCCAAGTCTCAATTAAGGTCAACAATCTT 546
538 GCAAGTGCATTTATGTTGATGCTTCCAGATTTATGCCAAGTCTCAATTAAGGTCAACAATCTT 597
547 TTTGTCGACCAACATGTTGAAGATGTTACATCTGTTGATCAATGAGGTTCTCCAGTAGT 606
598 TATGTCGACCAACATGTTGAAGATGTTACATCTGTTGATCAATGAGGTTCTCCAGTAGT 657
607 AACGGTGCATTTATGTTGATGCTTCCAGATTTATGCCAAGTCTCAATTAAGGTCAACAATCTT 666
658 ACTGGTGCATTTATGTTGATGCTTCCAGATTTATGCCAAGTCTCAATTAAGGTCAACAATCTT 717
667 GATTTGAATTTATCGGTTTCAATCTGAATCAATTTAGTTTACATTAAGGTCAACAATCTT 726
718 GATTTGAATTTATCGGTTTCAATCTGAATCAATTTAGTTTACATTAAGGTCAACAATCTT 777
727 GGAATTCAGATTAATCAAAATGATCTGCTGTTGATGTTGATGTTGATGTTGATGTTGAT 786
778 GGTATTTCTATCAATGAAATGTTGCTGTTGATGTTGATGTTGATGTTGATGTTGATGTT 837
787 ATTCTGCTACAGATGTTAAGCAATATATCTTTAGCATATACCAATGATGATGATGATGAT 846
838 ACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 894
847 GCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 906
895 GGTAGTCTCTTCAAAAGTAAAGCGTTTCAATTTAAGATTTGAGAGGATACAAATATAGTAA 954
907 GCGGATCTAAACGGTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 966
955 GCTAATTTCAACGGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1014
967 GCTGCTCACTACTTTACCATTTCAATCCAAAGTGTGATAAAACCAAAACCAATTCGAAATTTG 1026
1015 GCTGCTCACTACTTTACCATTTCAATCCAAAGTGTGATAAAACCAAAACCAATTCGAAATTTG 1074
1027 CAACCTATTCCAAACCTACCAATCAATCTTCAATTTGTTGTTGTTGTTGTTGTTGTTGTTG 1086
1075 CAACCTATTCCAAACCTACCAATCAATCTTCAATTTGTTGTTGTTGTTGTTGTTGTTGTTG 1134
1087 ACTAAGCTGCACCAATTTGGTGAACAGCTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1146
1135 ACTAAGCTGCACCAATTTGGTGAACAGCTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1194
1147 ACCAACAATGTTTACAGTGAAGGACAGGAAACCAATCACTACCAACCAACCACTGTTACCAAT 1206
1195 ACCAACAATGTTTACAGTGAAGGACAGGAAACCAATCACTACCAACCAACCACTGTTACCAAT 1245
1207 CCAACTGATTTCAATTCACACAGTGGTGGTACAGTTTCCA 1245
1255 CCAACTGATTTCTATAGTACTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1293

RESULT 6

US-10-245-802-13
; Sequence 13, Application US/10245802
; Publication No. US20030124134A1
; GENERAL INFORMATION:
; APPLICANT: Edwards, John E.

; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS TO VACCINATE AGAINST
; FILE REFERENCE: DISSEMINATED CANDIDIASIS
; CURRENT APPLICATION NUMBER: US/10/245,802
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 09/715,876
; PRIOR FILING DATE: 2000-11-18
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13

; LENGTH: 1407
; TYPE: DNA

; ORGANISM: Candida albicans
US-10-245-802-13

Query Match 58.9%; Score 733.4; DB 15; Length 1407;

Best Local Similarity 74.5%; Pred. No. 3.1e-155;

Matches 923; Conservative 0; Mismatches 316; Indels 0; Gaps 0;

QY 7 ATCACTGGTGTGTTTGTATGTTTAAATTCATTAACCTGGTCCAAATGCTGCTAATTTATGCT 66
DB 58 ATTACAGGTGTTTTCATAGTTTAAATTCGTTAACTTGGCCCAATGCTGCTTCTTATCCA 117
QY 67 TTCAAAGGCCAGGATACCCAACTTGGAAATGCTGTTTGGGTGGTCTTAGATGTGACC 126
DB 118 TATAGAGGTCCAGCTACTCTCTTCTGGACCGCTGTAATAGGATGCTTCTTAGATGAGCT 177
QY 127 AGTGCCAAATCCAGGGGATACATTCATTTGAATATGATGCTGCTGCTGCTGCTGCTGCTGCT 186
DB 178 ACTGCTAGTCTGGTGAACATTCACCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 237
QY 187 TCACAAACATCTGTTGATTTAACTCCGATGGTGTGTTAAATATGCTACTCTTGTCAATTTAT 246
DB 238 GATCAAAACGTCATTTGATTTAGTGTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 297
QY 247 TCTGCTGAAGATTCACAACTTTTCTACATTTAAACATGCTGCTGCTGCTGCTGCTGCTGCTGCT 306
DB 298 TCTGCGAAGAGTCTTACTACTCTTTTCTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 357
QY 307 TCATCCATTAAGGCAATTTGGTACAGTTACTTTTCAATTTGCAATTTCAATTTGCTGCTGCTGCT 366
DB 358 GCTGACACCAAGCCATAGGAATCTTAACATTTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 417
QY 367 GGTTCATCAACTGATTTGGAAGATTTCTAAATGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 426
DB 418 GGTTCAGATGTTGATTTGGCAATTTCTCAATGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 477
QY 427 TTTAATGATGCTGATAAAGATATCTCAATTTGATGTTGATGTTGATGTTGATGTTGATGTTGAT 486
DB 478 TTTAATGATGCTGATAAAGATATCTCAATTTGATGTTGATGTTGATGTTGATGTTGATGTTGAT 537
QY 487 CCAAGTGCATATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 546
DB 538 TCACGAGTCTGATCTGTTGTTGCTGCAAGATTTTACCAGTCTTTCACAGCAGTAAATCTT 597
QY 547 TTTGTCGACCAACATGTTGAAGATTTACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 606
DB 598 TTTCTTCCCAAGATGTCGAATGTTTATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 657
QY 607 AACGCTGAGTGTCTTATGATGCTTCAATTTGATGCTTCAATTTGATGCTTCAATTTGATGCTTCA 666
DB 658 GGTACTGCTGCTTACTATAGATTTGTTTCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 717
QY 667 GATTCGAATTTATCCGGTTTCTCTCAATCTCAATTTAGTTTACATTAAGGTCAACAATCTT 726
DB 718 GATTCGAATTTATCCGGTTTCTCTCAATCTCAATTTAGTTTACATTAAGGTCAACAATCTT 777

QY 727 GGAATTACAGATTAAATATCAAAATGTAACCTGGTATATCGTCCATTATTAATGATCTTAT 786
DB 778 AGTGTTTATAGTAATCTTTCAAAATGTTCTGCGGATATCGTCCATTATGATGCTTAT 837
QY 787 ATTTCTGCTACAGATGTTAAACCAATATATCTTTAGCATATACCAATGATATATCTTGCT 846
DB 838 ATTTCTGCAACAGAGTCAAGTCAATATACCAATGATATATATATATATATATGCTTGCT 897
QY 847 GGCAGTCTGCTGCAAAAGTAAACCTTTCACTTTAAGATGGAATGGAATGGAATGGAATGAT 906
DB 898 GCGCGGCTTCTGTTGAGTCACTCAATTTACTATCTATCTGCTGCGGATATAGTATATGCA 957
QY 907 GCGGATCTAAACGGTATTTGCTTTGCTGCTAACTAGAACAGTTACAGACAGTACACT 966
DB 958 GCTGGTTCTAATGTTATACCAATGTTGTTAACTAGAACAGTTACAGACAGTACACT 1017
QY 967 GCTGTCACACTTTACCAATTCGAATGTTGTTGATTAACCAACCAACCAATGGAATTTG 1026
DB 1018 GCTGTCACACTTTACCAATTCGAATGTTGATTAACCAACCAACCAATGGAATTTG 1077
QY 1027 CAACCTATTCCAACTACCACTACCACTCACTATGTTGTTGATGTTGTTGTTGTTGTTG 1086
DB 1078 CAACCTATTCCAACTACCACTACCACTCACTATGTTGTTGATGTTGTTGTTGTTGTTG 1137
QY 1087 ACTAAGACTGCAACAAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1146
DB 1138 ACTAAGACTGCAACAAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1197
QY 1147 ACCAAGCTGTTACCACTGATGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1206
DB 1198 ACTAAGCTGTTACCACTGATGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1257
QY 1207 CCAAGTATTCAATGTAACAGAGTGGTGGTAAAGTTCCA 1245
DB 1258 CCAAGTATTCAATGTAACAGAGTGGTGGTAAAGTTCCA 1296

RESULT 7

US-10-245-802-23
; Sequence 23, Application US/10245802
; Publication No. US20030124134A1
; GENERAL INFORMATION:
; APPLICANT: Edwards, John E.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS TO VACCINATE AGAINST
; TITLE OF INVENTION: DISSEMINATED CANDIDIASIS
; FILE REFERENCE: 013361.4003
; CURRENT APPLICATION NUMBER: US/10/245,802
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 09/715,876
; PRIOR FILING DATE: 2000-11-18
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 1404
; TYPE: DNA
; ORGANISM: Candida albicans
US-10-245-802-23

Query Match 57.3%; Score 713.8; DB 15; Length 1404;
Best Local Similarity 73.9%; Pred. No. 8.2e-151;
Matches 920; Conservative 0; Mismatches 322; Indels 3; Gaps 1;
QY 1 AAGCAATCACTGGTGTGTTTGTAGTATTTTAATTCATTAACTTGGTCCCAATGCTGCTAAT 60
DB 52 AAACTATATCTGGTGTGTTTCAATAGTTTGGTCACTCAATGACATGGAATGATCGGTTGAA 111
QY 61 TATGCTTTCAAGGCGCCAGGATACCCAACTTGGGAAGCTGTTTGGTGGTGGTGGTGGTGGT 120
DB 112 TATGCTTTCAAGGCGCCAGGATACCCAACTTGGGAAGCTGTTTGGTGGTGGTGGTGGTGGT 171
QY 121 GGTACCACTGCGCAATCCAGGGGATACATTCATATGATATGCCATGTTGTTAAATAT 180

DB 172 AGTACCCTGCTGACCCAGGAGACACATTCACCTTGATTTTGGCTTGTGTATTTAAATTT 231
QY 181 ACTACTTCAAAAATCTGTTGATTTAACTGCGGATGTTGTTAAATATATGCTACTTGTCAA 240
DB 232 ATAACTACCCAAACATCTGTTGATTTGATCTGCTGATGTTGATGCTATGCCCATTGTGAC 291
QY 241 TTTTATCTGTTGGAAGAATTCACAACTTTTCTACATTAACATGATGCTGTTGAACGACGT 300
DB 292 TTTAATGCTGGTGAAGAATTTACGACATTTTCTCTTATCATGCTGTTGAACGAGTGT 351
QY 301 TTGAATCATTCATTAAGGCAATTTGGTACAGTTACTTTTCAAAATGCAATTAATGTTGTT 360
DB 352 TCGGTATCATATGCTAGGTTTCTGTTACGGTCAAAATGCGCATTTACATTTCAATGTAGT 411
QY 361 GGAACAGGTTTCACTGATTTGGAAGATTTCTAAATGTTTACCTGCTGTTGTTGTTGTTG 420
DB 412 GGAACAGGTTTCTTCAATTTGTTGCGAATTTCCAAATGTTTACTGCGGGAATAAACACT 471
QY 421 GTCAATTTAATGATGGTGAATAAGATATCTCAATTTGATTTGTTGATTTGGAAGTCAACC 480
DB 472 GTGACTTTTCAATGATGGGATACAAAGATTTCTACCACTGTTGATTTTGAACGCTTCCA 531
QY 481 GTTGTATCCAAGTGCATATTTGTTATGCTTCCAGAGTTATGCTCAAGTCTCAATTAAGTCA 540
DB 532 GTATCAACCCAGTGGTTTATTAACAAGCTCACGAAATTTATTTCTTAGTCTCAATAACTTCA 591
QY 541 ACTCTTTTGTGCAACCAATGTTGGAAGTGTACACATCTGCTGTTGTTGTTGTTGTTGTTG 600
DB 592 AGTCTTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 651
QY 601 AGTAGTAAAGGTTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 660
DB 652 GCTATGTAACGGT---GCTACTATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 708
QY 661 TTAATGATTTGGAATTTATCCGGTTTCACTGTAATCAATTTAGTTTCACTTAAACTTGTACA 720
DB 709 TTAATGATTTGGAATTTTCCAGTAAAGTTTCCAGTAAAGTTTCACTTAACTTCACTGTAACG 768
QY 721 TCTAATGGAATTCAGATTTAAATATCAAAATGTTACCTGCTGTTGTTGTTGTTGTTGTTG 780
DB 769 TCAACCAAGTATTTACAGTTGGAATTTTCAAAATGTTTCTGCTGGGTATCGCCCTTTTGTG 828
QY 781 GCTTATATTTCTGCTACAGATTTAAACCAATATATCTTTAGCATATATCAATGATTTACT 840
DB 829 GCATATATTTCTGCGAAGAATTTTGAATATATCTTTCAGCTGACCAATGATGATACT 888
QY 841 TGTGCTGGCAGTCTGCTGCAAAAGTAAACCTTTTCACTTTTAAAGATGGAATGATGATCAAGA 900
DB 889 TGTGAAATGCGCAATATCTGTTGTTGATCCATTTTAACTGTTGGGGTATTAATAAC 948
QY 901 AGTATGCGGGATCTAAACGGTATTTGCTATTTGTTGCTTACCACTAGAACAGTTACAGACAGT 960
DB 949 TCTGAAGCAGACTCTGACGGGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATG 1008
QY 961 ACCACTGCTGCTACTACTTTTACCAATTCAAATGTTGATGTTGATGTTGATGTTGATGTTG 1020
DB 1009 ACAACAGCTGTGACTTACTTTACCTTTCAATTCCAAGTGTGATTAATAACCGAATAAC 1068
QY 1021 ATTTGCAACCTTATTCACCACTACATCACTTCACTATGTTGTTGTTGTTGTTGTTGTTGTT 1080
DB 1069 ATTTGCAACCTTATTCACCACTACATCACTTCACTATGTTGTTGTTGTTGTTGTTGTTG 1128
QY 1081 TATCTGATTAAGACTGCAACCAATTTGTTGAAACAGTACTGTTTATTTGTTGTTGTTGTTG 1140
DB 1129 TATGAACATTAACCGGAACATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1188
QY 1141 CATACTACCACTGTTTACAGTGAATGGAAGGAACTCACTACTACCACTCACTGTTGTTGTT 1200
DB 1189 CATATCACTGCTGTTTACAAATTTCTGAGCTGGGTCAATTTACCACTACCACTTACT 1248
QY 1201 ACCAATCCAACTGATTTCAATTTGACAGTGGTGGTACCAAGTTCCA 1245
DB 1249 ACTAATCCCACTGGTTCATAGACACTGTTTATTTGTTGCAAAATTTCCA 1293

RESULT 8
US-10-245-802-17
; Sequence 17, Application US/10245802
; Publication No. US20030124134A1
; GENERAL INFORMATION:
; APPLICANT: Edwards, John E.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS TO VACCINATE AGAINST
; TITLE OF INVENTION: DISSEMINATED CANDIDIASIS
; FILE REFERENCE: 013361.4003
; CURRENT APPLICATION NUMBER: US/10/245,802
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 09/715,876
; PRIOR FILING DATE: 2000-11-18
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 4332
; TYPE: DNA
; ORGANISM: Candida albicans
US-10-245-802-17

Query Match 46.2%; Score 574.6; DB 15; Length 4332;
Best Local Similarity 66.8%; Pred. No. 3.5e-119;
Matches 836; Conservative 0; Mismatches 409; Indels 6; Gaps 1;
QY 1 AAGACAATCACTGGTGTGTTTGTAGTATTTTAAATTCATTAACTTGGTCCAAATGCTGCTAAT 60
DB 55 AAAAATATATCGGGAGTTTTCAGAGTTTTCAGACTTTCAGCTTATGACCTATATCTAATACTGGTAAC 114
QY 61 TATGCTTCAAAAGGCGGATACCACTTGAATGCTGTTTGGTGGTCTTATGAT 120
DB 115 TACCAATATGCGGGTCTGCTGTTTCAACAATGAGCTGCTGTTTGGTGGAGCTGGAC 174
QY 121 GGTACCACTAGTCCAGGGATACATTCACATTCGAATATGCAATGCTGTTGTTAAATAT 180
DB 175 GGAACACTAGTCTAGTCCAGGTGATACATTTACATTTGTCATGCTGCTGCTTCAATTT 234
QY 181 ACTACTTCAAAACATCTGTTGATTTAACTGCGGATGTTGTTAAATATGCTACTGTCAA 240
DB 235 ATTACCAACAACACTTCAGTAGACTTAACTGCTAAATGCTGCTCAAGTATGCAACATGACT 294
QY 241 TTTTATCTGGTGAAGAAATTCACACTTTTCTACATTAACATGACTGCTGACGAGCT 300
DB 295 TTCCATGCGGGGAGACITTTACTCTTTTCAAGTATGAGTTGTTAGTAAATAATGG 354
QY 301 TTGAATCATCCATTAAAGGCAATTTGTTACAGTTTACTTTTACCAATTCATTTCAATTTGCT 360
DB 355 CTATCTTCAATATCAGAGGTTTGTACCGTCAAGCTACCAATTTCAATTCATTTGCT 414
QY 361 GGAACAGTTTCATCACTGATTTGGAAGATTTCAATGTTTACTGCTGCTGCTCAACATACA 420
DB 415 GGAACGTTTCTATCTGTCACATTTCAAGATTTCAAGTGTTCATCTGCTGCAACGACACT 474
QY 421 GTCAATTTATGATGCTGATTAAGATATCTCAATGATGTTGAGTTTGAAGTCAAC 480
DB 475 GTAACATTTACAGCGGATTCACAAATTTTCTACTACAGTCAATTTCCCTAAGACTCCA 534
QY 481 GTTGATCCAGTCAATTTGTTATGCTTCCAGAGTTTATGCAAGTCTCAATAGGTGACA 540
DB 535 GAATCATCTAGTAGCTGTTGTTATTTTCCAGAGGTTTATTCAGAGTCTGATTAATATCT 594
QY 541 ACTCTTTTGTGGCACCACATGTTGAAATGTTTACATCTGTTCAATGCGGTTCTCC 600
DB 595 AGTCTGTTGTTGCTTCTCAGTGTACTGCTGGATATGCAATCGGTGCTGCGATTTTCA 654
QY 601 AGTAGTACGGTGAAGTCTGATTTGATGCTCAATATTTCAATTTGTTGATTCACAAAGA 660
DB 655 GCAACAAAAGATGATGTGAATTTGATTTGTTTCTACTATACATGTTGGGAATAACAAATGT 714
QY 661 TTAATGATTTGGAATTTATCCGGTTTCTCATCTGAATCATTTAGTTTACACTAAATCTGTACA 720

DB 715 TTGAATAGTTGGATATGTCAGTATCATCAGAAATCAATTTTCTTACACCAAACTGTGACA 774
QY 721 TCTAATGGAATTCAGATTAAATATCAAAATGACCTGCTGGTTATCGTCCATTTATTTGAT 780
DB 775 CCAACAGTTTATTTATTTACTTATGAAATGTTCTCGCAGGTTATCGTCCATTTATTTGAT 834
QY 781 GCTT-----ATATTTCTGCTACAGATGTTAAACATATATCTTTAGCATATACCAATGAT 834
DB 835 TCTTAGTGAAATTAATCAGCAACAGCAATGGAATTTAAATTTGAATTACACGAATATA 894
QY 835 TATACTTGTGCTGGCAGTGTCTGCAAAAGTAAACCTTTTCACTTTAAAGATGGACTGGATAC 894
DB 895 TACAATTTGATGATGGCAAAAGGAATGATCTCTTATATATCTTTTGGACATCATAC 954
QY 895 AAGAATAGTATGCGGATCTAACGGTATTTGTCATTTGCTCAAACTAGAACAGTTTACA 954
DB 955 ACAATATGATGTCAGAGTCCAAATGAGCTGCGTAGTTGTTACTACGAGAACAGTCACT 1014
QY 955 GACAGTACCACCTGCTGTCTACTTACTTACCATTCAATCCAAAGTGTGATTAACCAACAA 1014
DB 1015 GATTTTACAACAGCAATTTACCACTTACCGTTTGTATCCCAAGTTGATTAACCAACAA 1074
QY 1015 ATCGAAATTTTGCACCTATTCCACCACTTACCATCACAACCTTTCATATGTTGTTGACT 1074
DB 1075 ATTGAATTAATGAAACCTTCTACTACCATTTACTTCTTATGTTGGATTTCT 1134
QY 1075 ACTTCTTATCTCACTAAGACTGCACCAATTTGGTGAACAGCTACTGTTTATTTGATGTG 1134
DB 1135 ACTTCACTTTCTACGAAGACTGCAACTATTGGAGGAACAGCAACTGTTGTTGATGTT 1194
QY 1135 CCATATCATCTACTACCACTGTTTACCAGTGAATGGCAGGAACATCACTACTACCACCA 1194
DB 1195 CCTATCATCAACATTTACCACTATCATAGTATATGAGTGGATCAGTACCACATCAAGT 1254
QY 1195 ACTCGTACCACCTTCCAACTGATTTCAATTTGACACAGTGGTGGTCAAGTTCCA 1245
DB 1255 ACTTATACAAATCCCCTGACTCGATTTGATACAGTTGTTGTTACAGTTCCA 1305

RESULT 9
US-10-245-802-19
; Sequence 19, Application US/10245802
; Publication No. US20030124134A1
; GENERAL INFORMATION:
; APPLICANT: Edwards, John E.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS TO VACCINATE AGAINST
; TITLE OF INVENTION: DISSEMINATED CANDIDIASIS
; FILE REFERENCE: 013361.4003
; CURRENT APPLICATION NUMBER: US/10/245,802
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 09/715,876
; PRIOR FILING DATE: 2000-11-18
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 6897
; TYPE: DNA
; ORGANISM: Candida albicans
US-10-245-802-19

Query Match 31.6%; Score 393.6; DB 15; Length 6897;
Best Local Similarity 57.8%; Pred. No. 2.9e-78;
Matches 721; Conservative 0; Mismatches 524; Indels 3; Gaps 1;
QY 1 AAGACAATCACTGGTGTGTTTGTAGTATTTTAAATTCATTAACTTGGTCCAAATGCTGCTAAT 60
DB 55 AAGAGATTAATCTGGTGTGTTTCAACCAATTCATTTGATATGCTTCTTACACATACAGA 114
QY 61 TATGCTTTCAAGGCGGACAGGATACCAACTTGGAAATGCTGTTTGGTGGTCTTCTTAGAT 120
DB 115 GCTCGATACGAAGAAATATCTACTTTACCGCTAATGCTCAATTTGGAATGGGCTTTGGAT 174
QY 121 GGTACAGTGCATCCAGGGGATACATTCATTTGAATATGCCATGTGTGTTTAAATAT 180

Db 175 GGTACTATTGCGAGTCCCGGTGATACATTTAATAGTATGCTCCCTGTGTATATAAATTC 234
Qy 181 ACTACTTCACAAACATCTGTGATTTAACTGCGGATGGTGTAAATATGCTACTTGTGCA 240
Db 235 ATGACGTAGCAAACTCAGTGCATTAATCTGCACTCTATTGCAATGCGCATGTGAC 294
Qy 241 TTTTATCTGGTGAAGAATTCACATTTTCTACATTAACATGATCTGTGACGACGCT 300
Db 295 TTGTGATGCTGGTGAAGACACTAAAGTTTCTCAAGTTTGAAGTGTACGCTGATGAG 354
Qy 301 TTGAATCATCATTAAGSCATTTGTGACAGTTTCTTACCAATGTCATTCATCTGCT 360
Db 355 TTGACAGAAATACAGCGTTTTTGAAGTGTATTTGCTTATTTGCTTTCATGTTGA 414
Qy 361 GGAACAGGTTTCATCACTGATTTGGAAGATTTCTAAATGTTTCTGCTGGTACCAATACA 420
Db 415 GGTTCGGGATCTAAATCTACGATAACAGACTCCAAATGTTTTCAAGTGGGTACAACT 474
Qy 421 GTCACATTTAATGATGGTGATTAAGATATCTCAATTTGATGTTGATTTGAAAGTCAACC 480
Db 475 GTCACGTTTTTTCAGCGGAACAATCAACTTTCTCAACTGCAAAATTTTCTCCCGAAGA 534
Qy 481 GTTGATCCAAGTGTCATATTTGTATGCTTCCAGTATGCGCAAGTCTCAATAGGTACA 540
Db 535 GAATGAGTTTTGCTGTAGTTGTAGTCAAGACTTTCCATGCTCGCTGATCAATGACT 594
Qy 541 ACTCTTTTTTGTGGCACCAATGTCGAAATGTTTACACATCTGGTACCAATGGGTTCTCC 600
Db 595 AATTTTGTATGCTACACCTTGTTCATGGGTATCAGCTGGGTAAAGTTAGTTTACA 654
Qy 601 AGTAGTACGGTGAGTTGCTATGATTTGCTCAAAATTTCTATTTGTTGGTATACAAAAGA 660
Db 655 TCTAATGATGATGATTTTGAATTTGAAATTTCTTCTATACATGTTGGTATAACTAATGA 714
Qy 661 TTAATGATGGAATTTATCCCGTTTCATCTGATCATTTAGTTACATCAAACTTTGTACA 720
Db 715 ATAATGATGGATGATGCCAGTATCTTCTGTTCCCTTCGATCATACTATAAGATGTACA 774
Qy 721 TCTAATGGAATTCAGATTTAAATATCAAAATGTACCTGCTGGTTATCGTCCATTTATTGAT 780
Db 775 TCAGTGACATTTACATTTAGTTTAAACAAATCTCTGAGGTATCGACCTTTTGTGAT 834
Qy 781 GCTTATATTTCTGCTACAGATGTTAAACCAATATCTTTAGCATATATCAATGATTAATCT 840
Db 835 GCGATTTGTTCAATACCAACGACAGACCTTTTTTGTAAATATATACAAATGAGTTTGGC 894
Qy 841 TGCTGTCAGTGGTCTGCAAGTAAACCTTTTCAC---TTTAAAGATGGAATGGATACAG 897
Db 895 TGTGTGAATGGATATACAGCTCCATACCTTTTCAAGTTTCTTCTCAGCCCAATTTTA 954
Qy 898 AATAGTATGCGGATCTTAACGGTATTTGCTATTTGCTCAACACTAGAACAGTTACAGAC 957
Db 955 TATGACGAGGCTTTAGCTATTTGTCAGACACCTAGTTGCTACCATCCACAGTGTAGGT 1014
Qy 958 AGTACCACTGCTGCTACATTTTACCATTTCAATCCAGTGTGTATGATAAAACCAAAATC 1017
Db 1015 TCCATTACCAAGCTACCAATTTACCTTTTCCGACTTCCAGAAAACCAAAACCAAT 1074
Qy 1018 GAAATTTTGAACCTATTTCACCACTACCACTCACTATGTTGTTGTTGCTACT 1077
Db 1075 CTAGTCTTAGAGCCCATACCCACCACTACGGTAAACCTTACACCACTGGCTTTGATCT 1134
Qy 1078 TCCTATCTGATAGACTGTCACCAATTTGGTGAACAGCTACTGTTATTGTTGATGTGCA 1137
Db 1135 TGGTATTATCTAGAAAGCCACCATTTGGTGACACAGCTACTGTTTCAATGATGTTCCA 1194
Qy 1138 TATCATCTACCACTGTTTACAGTGAATGGAAGGACCAATCACTACCAACCACT 1197
Db 1195 CAACATACAGCTACTCTTTGACCACTATTTGGCAAGAAATCAAGTACAGCGACCACT 1254
Qy 1198 CGTACCAATCCAACTGATTTCAATTTGACACAGTGGTGTACAGTTCCA 1245

Db 1255 TACTTCGATGACATAGACTTGGTCGATCTGCTCATTTGTTGAAAATTTCCA 1302
RESULT 10
US-09-864-761-2885
; Sequence 2885, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David K.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wenheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Ascomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 2885
; LENGTH: 436
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AP000018.2
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.4
US-09-864-761-2885

Query Match 4.4%; Score 55.4; DB 9; Length 436;
Best Local Similarity 48.6%; Pred. No. 0.014; Indels 0; Gaps 0;
Matches 152; Conservative 0; Mismatches 161; Indels 0; Gaps 0;

QY 914 CTAACGGTATGTGCTTGTGCTACCACTAGAACAGTTACAGACAGTACCACTGCTGCTCA 973
DB 68 CTATTGCTACTATTATACCACCTACCATAGTAGTACTACCACTCATCATCACTACCATCA 127

QY 974 CTACTTTACATTCATTCAGTGTGATGAACCAACCAACCAATTCGAAATTTTGCACCTTA 1033
DB 128 CTACTAATATCTATCATTCACCACTACTATTACCAATTCACCAAGTATCATTTACTACTA 187

QY 1034 TTCCACCACTACCATCAACCACTTATATGTTGGTGTGCTACTTCTCTGCTGCTAAGA 1093
DB 188 CCACCTCCACCATTAATCTACTACTAATGCTATCATTTACTACTGCTTCTATTAATTA 247

QY 1094 CTGCACCAATTTGTTGAAACAGCTACTGTTATTTGTTGATGTCATATCATCTACTACCA 1153
DB 248 CTCTACTCTCTACCATTAATCTACTACTAGTAGTATCACTACTACTACTACTATCA 307

QY 1154 CTGTTACCAAGTGAATGAGAGGAAACAACTACTACTACCACTCTGCTACCAATTCAC 1213
DB 308 CTATTACCAACCACTACTACTACTATCATTTACTACTACTACTACTACTACTACTACT 367

QY 1214 ATTCATTGACAC 1226
DB 368 CTGTCATTACTAC 380

RESULT 11
US-10-311-455-1075/c
; Sequence 1075, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining Cytosine Methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 1075
; LENGTH: 7758
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)

US-10-311-455-1075

Query Match 4.0%; Score 49.4; DB 13; Length 7758;
Best Local Similarity 47.7%; Pred. No. 1.3;
Matches 177; Conservative 0; Mismatches 191; Indels 3; Gaps 1;

QY 859 CAAAGTAACCTTTCACTTTAGATGAGTGGATGATACAGAAATAGTATCGCGATCTAAC 918
DB 6240 CCAACTACCCCTCTCTACTACACCAATATCTTCACTACCCCTCTACTACACCAATAT 6181

QY 919 GGTATTGCTATGTTGCTCACTAGAACAGTGTACAGACAGTACCACTGCTGCTACTACT 978
DB 6180 TCACTACCCCT 6121

QY 979 TTACCATTCATTCAGTGTGATGAACCAACCAACCAATTCGAAATTTTGCACCTATTCCA 1038
DB 6120 TCACTACCAACCTACTACTCTATAAACCACCACTACTCTCTCTCTCTCTCTCTCTCT 6061

QY 1039 ACCACTACCATCACCACTTCTATATGTTGGTGTGCTACTTCTCTATCTGACTAAGACTGCA 1098
DB 6060 CCAACTACCCCTCTCTACTACTCCAATATCTTCAACTTACCCCTCTCTCTCTCTCTCT 6001

QY 1099 CCAATTTGGTGAACAGTACTGTTATTTGTTGATGTCATATCATCTACTACTACCACTGTT 1158
DB 6000 CCAATTTACCCCTCTCTACTACTCCAATATCTTAACTACCCCTCTCTCTACTCTCA 5941

QY 1159 ACCAGTGA---ATGACAGGAAACATCTACTACCAACCACTGCTGCTACCAATCAACTGAT 1215
DB 5940 TCAACTACCCCTCTCTACTACTCTATAAATCTTAACTACTTCTCTCTACTACTTCA 5881

QY 1216 TCAATTGACAC 1226
DB 5880 TCAACTACCC 5870

RESULT 12
US-09-263-959-1
; Sequence 1, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UT
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 684973 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-09-263-959-1

Query Match 3.9%; Score 48.8; DB 10; Length 684973;
Best Local Similarity 46.2%; Pred. No. 17;
Matches 241; Conservative 0; Mismatches 272; Indels 9; Gaps 2;

QY 704 ACACATAAATTGTACATCTAATGGAATTCAGATTAAATATCAAAATGCTACTCTGCTGTT 763
DB 12574 ATACTACCCTGGCACTACTGATCTGTTCTCTATCACACCACTCTTTCCCAAGTACTA 12633

QY 764 ATGTCCTATTATTCATCTTATATTTCTGCTACAGATGTTAAACCAATATATCTTAGCAT 823
DB 12634 CTAGTTTACAACTAATATCTACTGTTCTGATACAACTCT---CTTTCCCTACAGTA 12690

QY 824 ATACCAATGATTATCTGCTGCGCAGTCTGCTGCAAGTAAACCTTTTCACTTTAAGAT 883
DB 12691 CTACTAATGCTAGCACTAATGCTACTGTTCTCTATCACACCACTCTTTCCCAAGTACTA 12750

Qy 884 GGACTGGATACAGAAATAGTATCGCGATCAACGGTATTGTCAATTTGCTCAACTA 943
Db 12751 CTATTTGGTTTACAACTAATCTACTGTTCCTCAATACAACTGCCCCCTTTCCCAACAATG 12810
Qy 944 GAACAGTTACAGACGATACCACTGCTG-----TCACCTATTACCAATCAATCAAGTG 997
Db 12811 CTAGTACTGTAGCACTAATGCTACTGTTCCTATACCAACACATGTTTTCGAACAAGTA 12870
Qy 998 TTGATAAAACCAAAACCAATCGAAATTTTGCACACCTATTCCAAACCACTACCACTCAACACTT 1057
Db 12871 CTATTTGGTTTACAACTAATGCTACTGTTCCTGATACAACTGCCCCCTTTCCCAACAATA 12930
Qy 1058 CATATGTTGGTGTGACTACTTCTATCTGATTAAGACGACCAATGTTGGTGAACAGCTA 1117
Db 12931 CTACTACTGTAGCACTAATGCTACTATTCTATACCAACCACTGTTTTCGAACAAGTA 12990
Qy 1118 CTGTTATGTTGATGTCATATCATATACCAACCACTGTTTACCAAGTGAATGGACGAA 1177
Db 12991 CTATTTAGTTTACAACTAGTACTACTGTTCCTGATACAACTGCTCTTTCCTCAAGTA 13050
Qy 1178 CAATCACTACCAACCACTGCTACCAATCCAACTGATTCAA 1219
Db 13051 CTACTAGTGTAGCACTAATGCTACTACCCCTGTTCTCTATACAA 13092

RESULT 13

US-10-363-798-1/c

; Sequence 1, Application US/10363798

; Publication No. US20030180280A1

; GENERAL INFORMATION:

; APPLICANT: Kong, Xiangyin

; APPLICANT: Xiao, Shangxi

; APPLICANT: Zhao, Guoping

; APPLICANT: Yu, Chuan

; APPLICANT: Hu, Landian

; TITLE OF INVENTION: METHOD OF DIAGNOSING AND TREATING DENTINOGENESIS IMPERFECTA

; TITLE OF INVENTION: TYPE II USING DENTIN SIALOPHOSPHOPROTEIN GENE AND CODED

; TITLE OF INVENTION: PRODUCT THEREOF

; FILE REFERENCE: 9548.78USWO

; CURRENT APPLICATION NUMBER: US/10/363,798

; CURRENT FILING DATE: 2003-03-05

; PRIOR APPLICATION NUMBER: CN 00125042.6

; PRIOR FILING DATE: 2000-09-05

; NUMBER OF SEQ ID NOS: 44

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 8201

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-363-798-1

Query Match 3.6%; Score 45.4; DB 13; Length 8201;
Best Local Similarity 45.2%; Pred. No. 11;
Matches 166; Conservative 0; Mismatches 201; Indels 0; Gaps 0;

Qy 184 ACTTCACAAACATCTGTTGATTAACTGCCGATGGTGTGTTAAATATGCTACTTGTCAATTT 243
Db 7119 ACTGCTATCACTGCTGCTCACTGCTATCGCTGTGCTGTGCTGCTGCTGCTGCTGCT 7060
Qy 244 TATTCCTGGTGAAGAAATTCACACTTTTCTACATTAACATGATGCTGTGTAACGACGCTTG 303
Db 7059 ATTGCTACTCACTGCTGCTCACTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTACT 7000
Qy 304 AAATCATCATTAAGGCATTTGGTACATTTCTTTTACCAATTTGCAATTCATTTGTTGTTGA 363
Db 6999 ATTACTGCTGCTCACTGCTATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTAT 6940
Qy 364 ACAGGTTTCATCACTGATTTGGAAGATTTCTAAATGTTTCTACTGCTGCTGCTGCTGCTGCT 423
Db 6939 GTTGTCACTACTATTACTGCTTTCCTGCTATCACTGCTGCTGCTGCTGCTGCTGCTGCT 6880
Qy 424 ACATTTAATGATGGTGATGAAGATATCTCAATGATGTTGAGTTGTTGAAAGATCAACCGTT 483

Db 6879 ACTGCTGTTGCTGCTATCACTGCTGCTCACTATCACTGCTGCTGCTGCTGCTGCTGCTG 6820
Qy 484 GATCCAAAGTGCATATTTGTTGATGCTTCCAGAGTTATGCCAAGTCTCAATAAGGTCACTACT 543
Db 6819 ACTGCTATTGCTGCTTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6760
Qy 544 CTTTGTG 550
Db 6759 GTTGTG 6753

RESULT 14

US-10-032-585-6880

; Sequence 6880, Application US/10032585

; Publication No. US20030180953A1

; GENERAL INFORMATION:

; APPLICANT: Terry, Roemer D.

; APPLICANT: Bo, Jiang

; APPLICANT: Charles, Boone

; APPLICANT: Howard, Bussey

; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery

; FILE REFERENCE: 10182-005-999

; CURRENT APPLICATION NUMBER: US/10/032,585

; CURRENT FILING DATE: 2001-12-20

; NUMBER OF SEQ ID NOS: 8000

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 6880

; LENGTH: 2280

; TYPE: DNA

; ORGANISM: Candida albicans

US-10-032-585-6880

Query Match 3.6%; Score 45; DB 13; Length 2280;
Best Local Similarity 46.2%; Pred. No. 6.9;
Matches 222; Conservative 0; Mismatches 255; Indels 4; Gaps 2;

Qy 631 TCAATATTCATATTGTTGTTATCACAAGAGTAAATGATGGAATATCCGGTT---TCA 687
Db 606 TCAATATTCACCAATTTGAAACATTTAATCATCCCAAGTCAAAATTTTCATTATGATTA 665
Qy 688 TCTGAATCATTTAGTTACACTTAAACCTTTGTACATCTAATGGAATTCAGATTAATATCA 747
Db 666 TGAACCGATTCAATGATATATTAAGAAATTAATTTGTAATTTAGAAATTAATATTT 725
Qy 748 AATGTAATCTGCTGTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 806
Db 726 CCCGAAATTTTCCAAATTTGATGATTTAATTAATTCATGATTTAATAATTTATGATGTA 785
Qy 807 CCATATATCTTAGCATATACCATGATATATCTTTGCTGGCAGTCTGCTGCAAGTAA 866
Db 786 TAAATTTGCTACTGGAGATATTTAATTTCCAAATGAATTAATAATTAATTAATTAATGT 845
Qy 867 ACCTTTTCACTTTAAGATGAGTGCATGATACAGAATAGTATGATGCGGATCTCAACGGTAT 926
Db 846 AAATCTACTGTTTTCCTCCATGCTATATATAATAATAAGAAAGTCCCTGGTGGAGG 905
Qy 927 CATTTGTTGCTAACTAGACAGTTACAGACGATACCACTGCTGCTGCTGCTGCTGCTGCTGCT 986
Db 906 AATGGAACAATAACTATATCATTTAGTTGAAATAGTACTATTGAAGAAGAATTAACAAG 965
Qy 987 CAATCCAGTGTGATTAACCAACCAACCAATTCGAAATTTTGCAACTATTTCACCCACTAC 1046
Db 966 AATTTCTTGGAAATGATATAACCAATTCATTTGAAATACCTTAAGTTGTTGATTAACAT 1025
Qy 1047 CATCACTACTTCATATGTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1106
Db 1026 ACGGACAAATTAACGAAATTTTAATAATTTTAACTCATATGCAATCAAAAGT 1085
Qy 1107 T 1107
Db 1086 T 1086

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 17, 2004, 21:05:28 ; Search time 2967 Seconds
(without alignments)
10198.542 Million cell updates/sec

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Perfect score: 1245
Sequence: 1 aagacaatcactgggtgtttt.....cagtggtgtacaagtcca 1245

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152338056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: em_estba.*

2: em_esthum.*

3: em_estin.*

4: em_estmu.*

5: em_estov.*

6: em_estpl.*

7: em_estro.*

8: em_hc.*

9: gb_estcl.*

10: gb_est2.*

11: gb_hc.*

12: gb_est3.*

13: gb_est4.*

14: gb_est5.*

15: em_estfun.*

16: em_estom.*

17: em_gss_hum.*

18: em_gss_inv.*

19: em_gss_pln.*

20: em_gss_vrt.*

21: em_gss_fun.*

22: em_gss_mam.*

23: em_gss_mus.*

24: em_gss_pro.*

25: em_gss_rod.*

26: em_gss_phg.*

27: em_gss_vrl.*

28: gb_gss1.*

29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
c 1	155	12.4	1047	29	CNS07D6L
c 2	139.4	11.2	1011	29	CNS07DAY
c 3	121.2	9.7	1050	29	CNS07CMQ
4	82.6	6.6	525	29	BZ351620
					AL440083 T7 end of
					AL440240 T7 end of
					AL439368 T7 end of
					BZ351620 hw04f06.g

c	5	80.4	6.5	735	29	CNS04NSM
c	6	80.2	6.4	843	29	BZ643413
	7	78.4	6.3	501	29	FR0048173
	8	77.6	6.2	513	29	BZ423698
	9	76.6	6.2	773	29	CNS01VTG
	10	75.8	6.1	480	29	BZ643398
	11	75.2	6.0	694	28	BH355163
	12	71.8	5.8	494	29	FR0048073
c	13	69.8	5.6	427	29	BZ423231
	14	69.6	5.6	350	28	BH879665
	15	69.6	5.6	989	29	CNS02H44
	16	68.6	5.5	334	29	BZ614791
	17	68.4	5.5	395	29	BZ316940
	18	67.8	5.4	989	29	CC149236
	19	67.6	5.4	356	29	CC171914
	20	66.6	5.3	423	29	BZ309688
	21	66.6	5.3	933	28	AZ204694
c	22	65.8	5.3	530	28	AZ166409
	23	65.4	5.3	306	29	BZ375744
	24	64.8	5.2	311	29	BZ638753
	25	64.6	5.2	320	29	BZ314341
	26	64	5.1	305	29	BZ333772
	27	63.6	5.1	428	12	BQ036742
	28	63.4	5.1	621	28	AZ164800
	29	62.6	5.0	914	28	AZ205202
c	30	62.4	5.0	810	28	AZ199472
	31	62.2	5.0	788	28	AZ183942
	32	61.8	5.0	266	29	BZ313584
	33	61.6	4.9	287	29	BZ644508
	34	61.2	4.9	619	29	FR0047601
	35	60.8	4.9	550	29	FR0043207
	36	60.4	4.9	450	29	FR0025683
	37	59.6	4.8	320	29	CC167070
	38	59.4	4.8	798	10	BF936821
	39	59.2	4.8	575	29	BZ780846
	40	59	4.7	289	29	BZ332780
	41	58.8	4.7	271	29	BZ310041
	42	58.8	4.7	500	28	B67199
	43	58	4.7	559	29	BX121516
	44	58	4.7	824	28	AZ185454
	45	57.6	4.6	305	29	BZ621988

ALIGNMENTS

RESULT 1
CNS07D6L/c

LOCUS

DEFINITION

1047 bp DNA linear GSS 08-JUL-2001
T7 end of clone BD0AA009H06 of library BD0AA from strain CBS 94 of
Candida tropicalis, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

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MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

TITLE	Genomic exploration of the hemiascomycetous yeasts: 16. <i>Candida tropicalis</i>
JOURNAL	FEBS Lett. 487 (1), 91-94 (2000)
MEDLINE	20584726
PUBMED	11152891
REFERENCE	3 (bases 1 to 1047)
AUTHORS	Genoscope.
TITLE	Direct Submission
JOURNAL	Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : seq@genoscope.cns.fr - Web : http://genoscope.cns.fr)
COMMENT	This GSS is part of a random genomic sequencing program of thirteen yeast species: <i>Saccharomyces bayanus</i> var. <i>uvarum</i> , <i>Saccharomyces exigius</i> , <i>Saccharomyces servazzii</i> , <i>Zygosaccharomyces rouxii</i> , <i>Saccharomyces kluyveri</i> , <i>Kluyveromyces thermotolerans</i> , <i>Kluyveromyces lactis</i> var. <i>lactis</i> , <i>Kluyveromyces marianus</i> var. <i>marianus</i> , <i>Pichia angusta</i> , <i>Debaryomyces hansenii</i> var. <i>hansenii</i> , <i>Pichia sorbitophila</i> , <i>Candida tropicalis</i> and <i>Yarrowia lipolytica</i> . Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

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FEATURES
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        1..1047
            Location/Qualifiers
                /organism="Candida tropicalis"
                /mol_type="genomic DNA"
                /strain="CBS 94"
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/ evidence="not experimental"
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ORIGIN					

Query Match	Score 155;	DB 29;	Length 1047;
Best Local Similarity	62.1%;		
	Pred. No. 3.2e-27;		
Marches 264. Conservative	0;	Mismatches 155;	Indels 6;
			Gaps 1;

[illegible]

427 AATATCTGGGATTTTAAATGATTTGAAATCTGTTTGGGTTGGTCTTAGAT 120
 62 -ATGCTTTCAAAGGGCCAGGATACCCAACTTTGGAATGCTGTTTGGGTTGGTCTTAGAT 120
 157 AGTCGATATCAAGGCTGATCAAAATTTCTTCACTGGGATCGAGAACTAAATGATTTTTCGAT 308

DG
QY

367 AGTGCATACAGAGA CCGCCHHTCCCTACTGTGGTTGGTTCATTCTCATTA
121 GGTACCAGTGCCCAATCCAGGGGATACATTCACATTGAATATGCCATGTGTGTTAAATAT 180

Db	307	GGAGAAATCTGCTGTAACCGAGTGATACATTTACATTAATTAATGCGATGTAATTCAAGTTC	248
Qc	181	ATCTACTTCAACAACAATCTCTTGATTTTAACTGCCGATGGTGTTAAATATGCTACTTGTCAA	240

247 ATTACAAATCAAAAACACTGTTGATTGATTGCTGATGGCACTACTTATCGACCTGTAAT 188

QY	241	TTTTATTCTGGTGAAGAAATTCACAACTTTTCTCTCATTTAACATCTACTCTGACGACGCT	300
Dh	187	CTCAAAATCTCGGAGAGAAATTTACTCTCTCTCAAGTTTAAAGCTCTACTCTTTTCATCTACC	128

QY 301 TTGAATCATCCATTAAAGCATTTGGTACAGTTACTTTACCAATTGCATTCAATGTTGGT 360

Db	127	TTGACAAATATACCCAGCTCGTGGTACTTTACATGTTCTCTTGACATTTAATGTGGGT	68
Ov	361	GGAAACAGGTTTCATCAACTGATTTGGGAAGATTTCTAAATGTTTTACTGCTGGTACCAATACA	420

67 AGTTCGGGAAC^{TT}CTGTGTTCTGTA^{CT}GACTGA^{TT}CTACTT^{CT}GCTT^{CT}CAGACCAGGTGTAA^{CA}CA^{CA} 8

Qy 421 GTCAC 425
 | | |
Db 7 GTAAC 3

RESULT 2	ACCESSION	ORGANISM
CNS07DAY	VERSION	
LOCUS	KEYWORDS	
DEFINITION	SOURCE	

REFERENCE

TITLE

JOURNAL
MEDICINE

REFERENCE

AUTHORS

TITLE

JOURNAL
MEDLINE

**PUBMED
REFERENCE
A1111093**

AUTHORS
TITLE
JOURNAL

Abstract

COMMENT

FEATURES

sources

major

FORM

	BASE COUNT	ORIGIN
0	100	100
1	90	90
2	80	80
3	70	70
4	60	60
5	50	50
6	40	40
7	30	30
8	20	20
9	10	10
10	0	0

Query Ma

Best Loc Matches

 $\alpha\gamma$

DB

CNS07DAY 1011 bp DNA linear GSS 08-JUL-2001
T7 end of clone BDOAA010H12 of library BDOAA from strain CBS 94 of
Candida tropicalis, genomic survey sequence.
AL440240
AL440240.1 GI:12233651
GSS
Candida tropicalis
Candida tropicalis.
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Mitosporic Saccharomycetales; Candida.
1 (bases 1 to 1011)
Souciet,J.L., Aigle,M., Artiguenave,P., Blandin,G.,
Boulotin,Fukuhara,M., Bon,E., Brottier,P., Cagaregola,S.,
de-Montigny,J., Dujon B., Durran,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
FEMS Lett. 487 (1), 3-12 (2000)
20584711
11152876
2 (bases 1 to 1011)
Blandin,G., Ozier-Kalogeropoulos,O., Wincker,P., Artiguenave,P. and
Dujon,B.
Genomic exploration of the hemiascomycetous yeasts: 16. Candida
tropicalis
FEMS Lett. 487 (1), 91-94 (2000)
20584726
11152891
3 (bases 1 to 1011)
Genoscope.
Direct Submission
Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Creteilux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
seqrefgenoscope.cns.fr - Web :
This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.

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FEATURES             Location/Qualifiers
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         /mol_type="genomic DNA"
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precursor, AUS1 ] [ Candida albicans]
1 putative frameshift(s)
/evidence=not experimental

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Best Local Similarity	65.0%		pred. No. 2.2e-23		
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ph	670	AAAGAAATTCGGGTGTGTCATAGGAATTCGAATCTTAACTTGGGATTAAGCTGGTAAAT	729		

Qy 61 TATGCTTTCAAGGCGGAGGATACCCAACTTGGAAATGCTGTTTGGGTGGTCTTAGAT 120
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 Qy 121 GGTACCAAGTGCATCCAGGAGATACATTCATTTGAATATGCCATGCTGTTTAAATAT 180
 Db 790 GGCACAACATCCCAAGGATGATGTTTCACTTTGATCATGCCCTGTGCTTCAAGTTC 849
 Qy 181 ACTACTTCAACAACATCTGTTGATTTAACTGCCGATGGTGTAAATATGCTACTTGTCAA 240
 Db 850 ACTACGTYTGCAATCTGTTTGGATCTGACTGCCAATGGKATGACATATGCCACATGTGAT 909
 Qy 241 TTTTAT-TCGTGGAGAATTCACACTTTTCTACATTAACATGATGTGAACAGCGC 299
 Db 910 CTTTCATGCCGGTGAAGAGTTTACTACTTACTTACTTACTTACTTACTTACTTACTTACTT 969
 Qy 300 TTTGAATATCATCCATTAAGGCATTTGGTA 328
 Db 970 GTTAAGTCTGTTTCATGAAGCTATGGGATA 998

RESULT 3

CNS07CMQ/c
 LOCUS
 DEFINITION T7 end of clone BD0AA004B02 of library BD0AA from strain CBS 94 of Candida tropicalis, genomic survey sequence.
 ACCESSION AL439368
 VERSION AL439368.1 GI:12222781
 KEYWORDS
 SOURCE
 ORGANISM
 Candida tropicalis
 Candida tropicalis
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; mitosporic Saccharomycetales; Candida.
 1 (bases 1 to 1050)
 Souciet J.L., Aigle M., Artiguenave P., Blandin G., Bolotin-Fukuhara M., Bon E., Brottier P., Casaregola S., de-Montigny J., Dujon B., Durrens P., Lepingle A., Liorente B., Malpertuy A., Neuvéglise C., Ozier-Kalogeropoulos O., Potier S., Saurin W., Tekala P., Toffano-Nioche C., Wesolowski-Louvel M., Wincker P. and Weissenbach J.
 Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
 FEBS Lett. 487 (1), 3-12 (2000)
 11152876
 2 (bases 1 to 1050)
 Blandin G., Ozier-Kalogeropoulos O., Wincker P., Artiguenave P. and Dujon B.
 Genomic exploration of the hemiascomycetous yeasts: 16. Candida tropicalis
 FEBS Lett. 487 (1), 91-94 (2000)
 20584726
 11152891
 3 (bases 1 to 1050)
 Genoscope.
 Direct Submission
 Submitted (08-SEP-2000) Genoscope - Centre National de Séquençage, 2 rue Gaston Crémieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: seqref@genoscope.cns.fr - Web: seqref@genoscope.cns.fr - Web: seqref@genoscope.cns.fr)
 This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES

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 /organism="Candida tropicalis"

/mol_type="genomic DNA"
 /strain="CBS 94"
 /db_xref="taxon:5482"
 /clone="BD0AA004B02"
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 /note="end : T7"
 complement (<7. >921)
 /notes="similar to O13368 [Agglutinin-like protein ALA1 precursor] [Candida albicans]"
 /evidence=not experimental
 misc_feature
 BASE COUNT 301 a 185 c 226 g 336 t 2 others
 ORIGIN

Query Match 9.7%; Score 121.2; DB 29; Length 1050;
 Best Local Similarity 61.3%; Pred. No. 7e-19;
 Matches 195; Conservative 0; Mismatches 123; Indels 0; Gaps 0;
 Qy 928 ATTGTTGCTACACTAGACAGTTACAGACAGTACCACTGCTGCTCACTACTTTACCAATTC 987
 Db 972 ATTGAAATCATCTACTAGAACAGTTACAGAACCACTACCTACGTTACCACTTTTACCATT 913
 Qy 988 AATCCAAAGTGTGATAAAACCAAAACCAATCGAAATTTTGCACACTTATCCCAACCACTACC 1047
 Db 912 GATTGAGCTACCCCAAGACAGACCAATTTGAATTTTAAACAATGCTTTTAAACAACA 853
 Qy 1048 ATCAACAATTCATATGTTGGTGTGACTACTTCTCTGACTAAGACTGCACCAATTTGGT 1107
 Db 852 ATAACAGGCTCATATGTGGTGTGTGACACACAGAAAGTACAACTTCTCTTTGTTACTTGA 793
 Qy 1108 GAAACAGCTACTGTTTATTTGTTGATGTCATATCACTACTACCACTGTTTACCACTGTTACCACTGAA 1167
 Db 792 GAGACTGCTACTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 733
 Qy 1168 TGACAGGAGCAACATCACTACCACTACCACTGTTTACCACTGTTTACCACTGTTTACCACT 1227
 Db 732 TGGATGAAGATACACTTCTACTTTGACAGTTATTTGATCCATCAGAACTATTGATACT 673
 Qy 1228 GTGGTGTACAAAGTTCCA 1245
 Db 672 GTGCTGTTGAATCATCCA 655

RESULT 4

BZ351620
 LOCUS
 DEFINITION hw04f06.g1 WGS-SbicolorF (JW107 adapted methyl filtered) Sorghum bicolor genomic clone hw04f06 5', genomic survey sequence.
 ACCESSION BZ351620
 VERSION BZ351620.1 GI:24915123
 KEYWORDS
 SOURCE
 ORGANISM
 Sorghum bicolor (sorghum)
 Sorghum bicolor
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.
 1 (bases 1 to 525)
 Rabinowicz P.D., O'Shaughnessy A.L., Balija V., Dedhia N., Katzenburger F., King L., Miller B., Muller S., Nascimento L., Zutavern T., Palmer L., McCombie W.R. and Martienssen R.A.
 Genomic shotgun sequences from Sorghum bicolor (methyl-filtered)
 Unpublished
 Contact: W. Richard McCombie
 Lita Annenberg Hazen Genome Sequencing Center
 Cold Spring Harbor Laboratory
 PO Box 100, Cold Spring Harbor, NY 11724, USA
 Tel: 516 367 8884
 Fax: 516 367 8874
 Email: mccombie@cshl.org
 Plate: hw04 row: f column: 06
 Seq primer: -21M13UnivRev
 Class: shotgun
 High quality sequence stop: 525.
 Location/Qualifiers
 FEATURES


```

source
1. 525
/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/db_xref="taxon:4558"
/clone="hw04f06"
/lab_host="JM107 or DH5a"
/clone_lib="WGS-Sbicolorf (JM107 adapted methyl filtered)"
/note="Site 1: Xba I; Site 2: Xba I; The vector was digested with Xba I and one nucleotide was added by fill in in the recessive 3' end. The genomic DNA was nebulized, end repaired, adaptor ligated and size fractionated using sephadex. The resulting fragments were between 0.8 and 3 kb and were cloned into the vector (Xba I) reads in M13mp19. b/g reads in pUC19. The same ligation was transformed in either JM107 or DH5a."
BASE COUNT 155 a 176 c 20 g 174 t
ORIGIN
Query Match 6.6%; Score 82.6; DB 29; Length 525;
Best Local Similarity 47.4%; Pred. No. 1.8e-09;
Matches 247; Conservative 0; Mismatches 274; Indels 0; Gaps 0;
Qy 706 ACTAAACTTGTACATCAATGGAATTCAGATTAAATATCAAAATGACCTGCTGTTAT 765
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 5 ACTACTGTCTACTACTACTGCTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 64
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 766 GGTCCATTATTGATGCTTATATTCTGCTACAGATGTTAACCAATATATCTTTAGCATAT 825
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 65 ACTACTGTCTACTGCTGCTACTGCTGCTACTGCTGCTACTGCTGCTACTGCTACT 124
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 826 ACCAATGATTATCTTGTGCTGGCAGTGTCTGCAAGTAACCTTTCACTTTAAGATGG 885
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 125 ACTGCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 184
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 886 ACTGATACAGATAGTATGATGCGGATCTACGATATGTCATTTGCTTACCACTAGA 945
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 185 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 244
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 946 ACAGTTACAGACGTACCCTGCTGCTCACTACTCTTTACCAATTCATTCGAAGTGTGNTAAA 1005
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 245 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 304
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1006 ACCAAACAAATCGAAATTTTGGACCTATTTCACCACTACATCAATCACTTATGTT 1065
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 305 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 364
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1066 GGTGTGACTCTTCTATCTGATTAAGACTGCACCAATTTGGTGAACAGCTACTGTTATT 1125
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 365 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 424
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1126 GTTGATGTGCCATATCATCTACCACTGTTTACAGTGAATGGACAGCAATCACT 1185
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 425 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 484
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1186 ACCACCACTCGTACCAATCCAACTGATTCATTAATGACAC 1226
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 485 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 525
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 5
CNS04NSM/c 735 bp DNA linear GSS 01-SEP-2000
LOCUS Tetraodon nigroviridis genome survey sequence T7 end of clone
DEFINITION 123M05 of library G from Tetraodon nigroviridis, genomic survey
sequence.
AL299119
AL299119.1 GI:8038260
GSS: genome survey sequence.
KEYWORDS Tetraodon nigroviridis
SOURCE Tetraodon nigroviridis
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

REFERENCE
AUTHORS Roest Crolius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, P.,
Saurin, W. and Weissenbach, J.
TITLE Estimate of human gene number provided by genome-wide analysis
using Tetraodon nigroviridis DNA sequence
JOURNAL Nat. Genet. 25 (2), 235-238 (2000)
MEDLINE 20296633
PUBMED 10835645
AUTHORS Roest Crolius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C.,
Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, P.,
Saurin, W., Bernot, A. and Weissenbach, J.
TITLE Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
JOURNAL Genome Res. 10 (7), 939-949 (2000)
MEDLINE 20359837
PUBMED 1089143
AUTHORS Roest Crolius, H., Jaillon, O., Dasilva, C., Bouneau, L., Billault, A.,
Quetier, P., Saurin, W., Bernot, A. and Weissenbach, J.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 131 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
COMMENT - Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
FEATURES
source
1. 735
/organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="123M05"
/clone_lib="G"
/note="Genoscope sequence ID : COBG123AG03LP1-end : T7"
BASE COUNT 242 a 45 c 223 g 197 t 28 others
ORIGIN
Query Match 6.5%; Score 80.4; DB 29; Length 735;
Best Local Similarity 47.4%; Pred. No. 7e-09;
Matches 251; Conservative 6; Mismatches 272; Indels 1; Gaps 1;
Qy 699 TAGTTACATCAAACTTTGTACATCTAATGGAATTCAGATTAAATATCAAAATGCTACCTGC 758
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 530 TACTGTCAAACTACTACTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 471
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 759 TGGTTATCGTCCATTATTGATGCTTATATTTCTGCTACAGATGTTAAACCAATATCTTT 818
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 470 TGCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 411
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 819 AGCATATACCAATGATTATATCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 878
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 410 TGCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 351
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 879 AAGATGCACTGGATACAAGAATAGTATGATGCGGATCTAAGCGGTATGTCATTTGTTGCTAC 938
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 350 TACTACTACTTTTCTACTGCTACTACTACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 291
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 939 AACTAGAACAGTTTACAGACAGTACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 998
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 290 TACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 231
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 999 TGTATAAACCAAAACCAATCGAAATTTTGCACCTATTTCACCACTACCTACCACTCCTC 1058
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 230 TACTGCTGCTACTACCACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 171
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1059 ATATGTTGGTGTGACTATCTTCCTATCTGACTAGACTGACCACTTGGTGAACAGCTAC 1118
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 170 TACTGCTGCTACTACCACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 111
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1119 TGTATTGTTGATGTGCTGCATATCA-TACTACCACAACTGTTTACCAGTGAATGGACAGAA 1177
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Db | | | | | | | | | | | | | | | | | |
110 TACTACTGCTGCTACTTACTACTACTACTGCTGCTACTGCTACTGCTACTGCTA 51

QY | | | | | | | | | | | | | | | | | |
1178 CAATCATTACCACCACTCGTTACCACTCCAACTGATTCATTTGCACA 1227

Db | | | | | | | | | | | | | | | | | |
50 CTACTACTACTACTACTACTACTACTACTACTGCTACTACTACTASTACA 1

RESULT 6					
BZ643413/c					
LOCUS	BZ643413	843 bp	DNA	linear	GSS 29-JAN-2003
DEFINITION	CGAOW57TM_ZM_0.7_1.5_KB_Zea mays genomic clone ZM95Ma011J17,				
	genomic survey sequence.				

ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
B2643413	B2643413.1	GI:28104915	Zea mays	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
	GSS.		Zea mays	

REFERENCE	AUTHORS	TITLE
1 (bases 1 to 843)	Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.	Consortium for Maize Genomics

JOURNAL COMMENT
Unpublished
Other GSSs: OGAOW57TC
Contact: Cathy Whitelaw
TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.

```

FEATURES
    source
        Location/Qualifiers
            1. .843
                /organism="Zea mays"
                /mol_type="genomic DNA"
                /strain="B73"
                /db_xref="taxon:4577"
                /clone="ZMBWA011J17"
                /clone_lib="ZM 0.7 1.5_KB"
                /note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
                    methylation filtered genomic DNA library"
            281 a 125 c 279 g 158 t

```

Query Match	6.4%	Score 80.2;	DB 29;	Length 843;
Best Local Similarity	45.7%;	Pred. No. 8.2e-09;		
Matches 280;	Conservative	0;	Mismatches 333;	Indels 0;
			Gaps	0;

616 GTTGTATTGATGTCCTCAAAATATTCTATTTCTGTTATCAGAAAAAGGATTAATGATTGGAAAT 675
 |||||
 792 GCTACTACTGCTACTACTGCTGCTGATGCTGCTACTGTGCTACTGTGCTACTGTGCTACT 733
 |||||

676 TATCGGTTTCATCTGAATCAATTAGTTACATAAATCTTGACATCTAATGAATTCAG 735
732 ACTGCTACTGTCGGCTACTCTGCTACTCTGCTGCTCTATCTATCTATTCACGCTCATCTCTCTGCTACT 573

732 ACATGCTACATGCTACATGCTACATGCTACATGCTACATGCTACT 673

736 ATTAATAATCAAAATGTACCTCTGCTTATCTGTCATTTATGATGCTATATTTCTGT 795

739 TCTTTCTGCTTATGATGCTATATTTCTGT 795

672 ACTACTGCTACTGCTACTACTACTGCTACTGCTACTGCTACTGCTACTGCT 613

796 ACAGATGTTAACCAATATACCTTTAGCATATACCAATGATTATATCTTGCTGCTGGCAGTCGT 855

612 ACTGCTGCTATTGCTGCTACTCCAGTACTCTGCTGTGCTGCTGCTGCTACT 553

856 CTGCAAAAGTAAACCTTTTCACTTTTAGATGGACCTGGATACAAGATAGTGGCCGGATCT 915

dbb
552 GCTACTGCTGTA CTGCTGTCTACTACTGCTGCTACTGCTGCTACTACT 493

Qy	916	AACGGTATTGCTANTGTTGCTCAACTAGAACAGTTACAGACAGTACCACTGCTGCACCT	975
Db	492	GCTACTACTGCTACTGCTGCTGCACTGCTACTGCTACTGCTACTACTACTACT	433
Qy	976	ACTTTTACCATTCAATCCAAAGTGTGATAAAACCAAAACAATCGMAATTTTGGCAACCTATT	1035
Db	432	GCITGCTGCTACTACTACTGCTAAATGCTACTACTACTGCTGCTACTACTACTACT	373
Qy	1036	CCAAACCACTACCAATCACACATTCATATGTTGGTGTGCACTACTTCCCTATCTGACTAAGACT	1095
Db	372	GCTCCTACTACTGCTACTACTGCTACTGCTTCTACTACTACTACTGCTACTGCTACTGCT	313
Qy	1096	GCACCAATTGGTGAACACGCTACTGTTATTGTTGTGATGTGCCATATCATACTACCACAACT	1155
Db	312	ACTGCTACTGCTACAGCTACTACAGCTACTACTGCTACTCTCTGCTACTACTGCTACT	253
Qy	1156	GTTTACCAAGTATGACACAGGAACATCACTACCACCAACTCGGTACCAATCCAACTGAT	1215
Db	252	ACTACTACTGCTACTACTGCTACTACTACTGCTACTACTGCTACTACTGCTACTGCT	193
Qy	1216	TCAATTGACACAG	1228
Db	192	ACTGCTGCTACTG	180

RESULT 7	
FR0048173	
LOCUS	501 bp DNA linear GSS 05-JAN-2001
DEFINITION	Fugu rubripes GSS sequence, clone 264E22ca9, genomic survey sequence.

ACCESSION	AL444958	
VERSION	AL444958.1	GI:12053458
KEYWORDS	GSS; genome survey sequence.	
SOURCE	Takifugu rubripes	
ORGANISM	Takifugu rubripes	

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetrodontiformes; Tetracantoidea; Tetracantidae; Takifugu.

REFERENCE
AUTHORS
TITLE
JOURNAL

biohelp@gmp.mrc.ac.uk
Vector: pBluescript II KS
V_Type: phagemid
PRIMER: KS
DESCR:

DESCRIPTORS: One pass dye-terminator sequencing of BAC (pBelobACII) cloned genomic sequence
The BACs can be obtained from <http://www.incyte.com>.

```

FEATURES
  source
    Location/Qualifiers
      1..501
        /organism="Takifugu rubripes"
        /mol_type="Genomic DNA"
        /db_xref="taxon:31033"
        /clone="264E22CA9"
        /clone_lib="BAC 264E22"
      132 a 161 c 35 g 173 t
        BASE COUNT

```

Query Match 6.3%; Score 78.4; DB 29; Length 501;
Best Local Similarity 47.9%; Pred. No. 1.9e-08;
Matches 226; Conservative 0; Mismatches 246; Indels 0; Gaps 0;

755	CTGTGGTTATCGTCCATTATTGATGCTTATATTTCTGCACAGATGTTAAACCAATATA	814
19	CTGTGCTTCTACTACTGCTACTACTACTACTCTGCTACTACTGCTGCTTCTACTA	78
815	CTTTTACATATACCAATGATTAATACTTGTGCTGSCAGTCGTGCAAAAGTAAACCTTTCA	874
79	CTACTACTACTACTGCTACTACTACTACTGCTACTACTACTACTACTACTACTGCTG	138

```

ORIGIN
Query Match      6.2%; Score 77.6; DB 29; Length 513;
Best Local Similarity 47.0%; Pred. No. 3e-08;
Matches 239; Conservative 0; Mismatches 269; Indels 0; Gaps 0;

QY 875 CTTTAAAGTAGGACTGATACAGAAATAGTAGGATGCGGATCTAAACGGTATTTGTCATGTTG 934
DB 139 CTGCTTCTACTACTGCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 198

QY 935 CTACAACTAGAACAGTTACAGACAGTACCACTGCTGCTACTACTACTACTACTACTACTACT 994
DB 199 CTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 258

QY 995 GTGTTGATAAACCACCAACCAATCGAAATTTTGCACCTATTCCAAACCACTACTACACAA 1054
DB 259 CTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 318

QY 1055 CTTTCATATGTTGGTGTGACTACTCTCTATCTGACCTAAGACTGCACCAATTTGGTGAACAG 1114
DB 319 CTTTCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTGTA 378

QY 1115 CTACTGTTATTTGTTGATGCGCATATCATACTACCACTGTTACCACTGTAATGGACAG 1174
DB 379 CTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 438

QY 1175 GAACAACTACTACCAACCACTCGTACCAATCCAACTGATTCAAATTCACAC 1226
DB 439 CTGCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 490

```

```

RESULT 8
LOCUS BZ423698 513 bp DNA linear GSS 10-DEC-2002
DEFINITION id52c10.g1 WGS-SbicolorP (DH5a methyl filtered) Sorghum bicolor
genomic clone id52c10 5', genomic survey sequence.
ACCESSION BZ423698
VERSION BZ423698.1 GI:26373196
KEYWORDS GSS.
SOURCE Sorghum bicolor (sorghum)
ORGANISM Sorghum bicolor
REFERENCE Rabinowicz, P.D., O'Shaughnessy, A.L., Ballia, V., Dedhia, N.,
AUTHORS Katsenburger, F., King, L., Miller, B., Muller, S., Nascimento, L.,
Zutavern, T., Palmer, L., McCombie, W.R. and Martienssen, R.A.
TITLE Genomic shotgun sequences from Sorghum bicolor (methyl-filtered)
JOURNAL Unpublished
COMMENT Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Plate: id52 row: c column: 10
Seq primer: -21M13UnivRev
Class: shotgun
High quality sequence stop: 513.
Location/Qualifiers
1..513
/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/db_xref="taxon:4558"
/clone="id52c10"
/lab_host="DH5a"
/notes="Site 1: Xba I and one nucleotide was added by fill in
digested with XbaI and one nucleotide was added by fill in
in the recessive 3' end. The genomic DNA was nebulized,
end repaired, adaptor ligated and size fractionated using
sephadex. The resulting fragments were between 0.8 and 3
kb and were cloned into the vector (.x/y reads in M13mp19,
b/g reads in pUC19). The same ligation was transformed
into DH5a."
153 a 169 c 20 g 171 t

```

```

FEATURES
source
1..513
/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/db_xref="taxon:4558"
/clone="id52c10"
/lab_host="DH5a"
/notes="Site 1: Xba I and one nucleotide was added by fill in
digested with XbaI and one nucleotide was added by fill in
in the recessive 3' end. The genomic DNA was nebulized,
end repaired, adaptor ligated and size fractionated using
sephadex. The resulting fragments were between 0.8 and 3
kb and were cloned into the vector (.x/y reads in M13mp19,
b/g reads in pUC19). The same ligation was transformed
into DH5a."
153 a 169 c 20 g 171 t

```

```

ORIGIN
Query Match      6.2%; Score 77.6; DB 29; Length 513;
Best Local Similarity 47.0%; Pred. No. 3e-08;
Matches 239; Conservative 0; Mismatches 269; Indels 0; Gaps 0;

QY 706 ACTAAAACTTGTCATCTAAATGGAATTCAGATTAAATATCAAAATGTACCTGCTGGTTAT 765
DB 6 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 65

QY 766 CGTCCATTTATGATGCTATATTTCTGCTACAGATGTTAAACCAATATATATTTAGCATAT 825
DB 66 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 125

QY 826 ACCAATGATATATCTGCTGCGCAGTGGCTGCAAAAGTAAACCTTTTACATTTAAGATGG 885
DB 126 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 185

QY 886 ACTGATACAGAAATAGTAGCGGATCTAAACGGTATTTGTCATTTGTTGCTACAACTAGA 945
DB 186 AGTGTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 245

QY 946 ACAGTTACAGACAGTACCACTGCTGCTACTACTTTTCAATTCAAATCCAAAGTTGATAAA 1005
DB 246 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 305

QY 1006 ACCAAACCAATCGAAATTTTGCACCTATTCACCACTACTACCACTTTCATATGTT 1065
DB 306 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 365

QY 1066 GGTGTGACTACTTCTCTATCTGACTAAGACTGCACCAATTTGGTGAACAGTACTGTTAT 1125
DB 366 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 425

QY 1126 GTTGATGCGCATATCATACTACCAACTGTTTACCAGTGAATGACAGGAACATCACT 1185
DB 456 GCTGTGCTACTACTACTACTGCTGCTACTACTACTACTACTACTACTACTACTACTACTACT 485

QY 1186 ACCCAACCACTCGTACCAATCCAACTG 1213
DB 486 GCTACTACTACTACTACTACTACTACTG 513

RESULT 9
LOCUS CNS01VTG 773 bp DNA linear GSS 01-SEP-2000
DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone
199C24 of library G from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION AL169549
VERSION AL169549.1 GI:7807606
KEYWORDS GSS; genome survey sequence.
SOURCE Tetraodon nigroviridis
ORGANISM Tetraodon nigroviridis
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Tetraodon.
1 Roest Crolius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bertot, A., Fzames, C., Wincker, P., Brottier, P., Quetier, P.,
Saurin, W. and Weissenbach, J.
Estimate of human gene number provided by genome-wide analysis
using Tetraodon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
20296633
10835645
JOURNAL MEDLINE
PUBMED
REFERENCE
AUTHORS Roest Crolius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C.,
Fzames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, P.,
Saurin, W., Bertot, A. and Weissenbach, J.
TITLE Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis

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JOURNAL MEDLINE
PUBMED 20359837
REFERENCE 3 (bases 1 to 773)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seque@genoscope.cns.fr)
- Web : www.genoscope.cns.fr

COMMENT
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/tetraodon>.

FEATURES
source
1..773
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/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="199C24"
/clone_lib="G"
/notes="Genoscope sequence ID : COAG199BB12LP1-end : T7"
BASE COUNT 210 a 265 c 69 g 184 t 45 others
ORIGIN

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Best Local Similarity 41.5%; Pred. No. 6.2e-08;
Matches 253; Conservative 31; Mismatches 325; Indels 0; Gaps 0;

QY 618 TGCATTGATGCTCAATATTCATATTTGGTATCACAAGGATTAATGATTCGAATTA 677
DB 161 TGATCTGCTACTACTACWCTGCTACWAGTGTGACWAGCTACTGCTACTGCTAC 220

QY 678 TCCGGTTTCATCTGAATCAITTAGTACACTAAAACCTTTGATCTACTAATGGAATTCAGAT 737
DB 221 TACTACTAGTCTACTACTGCTACTGCTACTACTGCTACTACTACWAGTGTCTACTGCTAC 280

QY 738 TAAATATCAAAATGCTGCTGTTATTCGTCATTTATTTGATGCTTATTTCTGCTAC 797
DB 281 TGCTACTACWACTGCTGCTACTGCTGCTACTACTACTACTACTACTACTACTACTACT 340

QY 798 AGATGTTAAACCAATATCTTTAGCATATATCAATGATTTATTTGCTGCTGCTGCTCT 857
DB 341 TACTACTACTACTACTACTACTGCAWACCAAGCATATCTACTGCTACTACTACTGCT 400

QY 858 GCAAGTAAACCTTTTCACTTTAAGATGCACTGGATACAGAAATAGTATGATGCGGATCTAA 917
DB 401 ACATCTGCAACTACWCACTGCACTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 460

QY 918 CGGTATTTGCTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 977
DB 461 WRWCAWCACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 520

QY 978 TTTACCAATCAATCAAGTGTGTGATAAACCACCAATCGAAATTTTGCAACCTATTC 1037
DB 521 TRCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 580

QY 1038 AACCACTACCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1097
DB 581 WACTGCTACWACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 640

QY 1098 ACCAATTTGGTGAACAGCTACTGTTATTTGATGCTGCTGCTGCTGCTGCTGCTGCT 1157
DB 641 ACTACACATACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 700

QY 1158 TACCAGTGAATGGACAGCAATCACTACCAACCAACCACTGCTGCTGCTGCTGCTGCT 1217
DB 701 TACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 760

QY 1218 AATTGACAC 1226
DB 761 TACTGCTAC 769

RESULT 10
BZ643398
LOCUS BZ643398 480 bp DNA linear GSS 29-JAN-2003
DEFINITION OGAOW57TC ZM 0.7 1.5 KB Zea mays genomic clone ZMMBMA011J17,
genomic survey sequence.
ACCESSION BZ643398
VERSION BZ643398.1 GI:28104877
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 480)
AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick
A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T., Citek
R.W., Nunberg,A., Robbins,D. and Lakey,N.
TITLE Consortium for Maize Genomics
JOURNAL Unpublished
COMMENT Other_GSSs: OGAOW57TM
Contact: Cathy Whitelaw
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TP
Class: sheared ends.

FEATURES
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/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
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methylation filtered genomic DNA library"
BASE COUNT 96 a 160 c 65 g 159 t
ORIGIN

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Best Local Similarity 47.8%; Pred. No. 8e-08;
Matches 224; Conservative 0; Mismatches 247; Indels 0; Gaps 0;

QY 756 TGTCTGTTATCGTCCATTTTATGATGCTTATTTCTGCTACAGATGTTAACCAATATAC 815
DB 1 TGCTACTGCTGCTACTGCTACTACTACTACTGCTGCTGCTGCTGCTGCTGCTGCTAC 60

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DB 61 TGCTACTGCTGCTACTACTACTACTACTACTGCTGCTGCTGCTGCTGCTGCTGCTAC 120

QY 876 TTTAAGATGAGCTGGATACAGAAATAGTGTGATCGCGGATCTAACGGTATTTGCTATTGTTGC 935
DB 121 TACTACTGCTGCTACTACTACTACTACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180

QY 936 TACCACTAGAACAGTTTACAGACAGTACCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 995
DB 181 TACTACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240

QY 996 TGTGTATAAAACCAAAACAAATCGAAATTTTGGAACTTTTCCAAACCACTACCAATCAAC 1055
DB 241 TACTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300

QY 1056 TTCATATGTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1115
DB 301 TACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360

QY 1116 TACTGTTATTTGTTGATGCTGCCATATCATACTACCAACTGTTTACCAGTGAATGACAGG 1175
DB 361 TACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420

QY 1176 AACATCACTACCAACCACTGCTGATCAATCCAACTGATTCATTCAGAC 1226
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 Db 421 TACTACTGCTACTGCTGCTACTGCTACTGCTACTGCTACTGCTACT 471
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RESULT 11
 BH355163
 LOCUS CH230-81P6.TJ CHORI-230 Segment 1 Rattus norvegicus genomic clone
 DEFINITION CH230-81P6, genomic survey sequence.
 ACCESSION BH355163
 VERSION BH355163.1 GI:17285897
 KEYWORDS GSS.
 ORGANISM Rattus norvegicus (Norway rat)
 SOURCE Rattus norvegicus
 ORGANISM Rattus norvegicus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 694)
 Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn
 A., Gebregorgis, E., Overton, L., Russell, D., Chen, D., Riggs, P., de
 Jong, P. and Fraser, C.M.
 Rat BAC End Sequences from Library CHORI-230 BcoRI segment
 Unpublished
 Other GSSs: CH230-81P6.TV
 Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org
 Clones are derived from the rat BAC library CHORI-230
 (http://www.chori.org/bacpac/rat230.htm). For BAC library
 availability, please contact Pieter de Jong (pdejong@mail.choi.org).
 Clones may be purchased from BACPAC Resources
 (http://www.chori.org/bacpac/orering/information.htm). BAC end
 page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
 Plate: 81 row: P column: 6
 Seg primer: SP6
 Class: BAC ends.
 Location/Qualifiers
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 /note="Vector: pTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI;
 CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by
 Pieter de Jong"

FEATURES
source

BASE COUNT 270 a 160 c 53 g 211 t
 ORIGIN
 Query Match 6.0%; Score 75.2; DB 28; Length 694;
 Best Local Similarity 48.2%; Pred. No. 1.3e-07;
 Matches 241; Conservative 0; Mismatches 258; Indels 1; Gaps 1;

QY 687 ATCTGAATCATTTAGTACATAAACTTGATCTTAATGGAATTCAGATTAATCA 746
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 Db 192 AGCAGCAGTACTACTACTACTACTACTACTACTACTACTACTACTACTACTAA 251
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QY 747 AAATGACTCTGCTGATCGTCATTTATTGATGCTTATTTCTGCTACAGATGTTAA 806
 |||||
 Db 252 TAATATTACTACTACTCAAGTACTACTATCACTAC-TACTACTATTACTACTAC 310
 |||||

QY 807 CCATATATCTTAGCATATACCAATGATTATATGCTGTCGAGTCGTCGCAAGTAA 866
 |||||
 Db 311 TAAACTACTACTACTAATATATATATATATATATATATATATATATATATAC 370
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QY 867 ACCTTTCATTTAAGATGGAGTGGATACAGATAGTATGCGGATCTAACGGTATTGT 926
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 Db 371 TACTACTACTACTATTACTTGCTACTACTACTCAAGTACTACTATTACTTGCTACAAC 430
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QY 927 CATTTGTTGCTACAACTAGAACAGTTTACAGACAGTACCACTGCTGTCTACTTTCACATT 986
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 Db 431 TACTATTACTACTACTACTACTACTACTACTACTAAACTACTACTATTACTACTACAAC 490
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QY 987 CAATCCAACTGTTGATATAAAACCAAAACAATCGAAATTTGGCAACCTATTCCCAACCACTAC 1046
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 Db 491 TACTACTACTGTTATTACTACTACTACTAAAACTACTACTATTACTACTACTATTACTATTAC 550
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 Db 551 TACTACTACTACTCAAGTACTACTATTACTACTACTATTACTACTACTACTACTACTAT 610
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QY 1107 TGAACACGCTACTGTTATTGTTGATGTGCATATCATCTACTACCAACTGTTTACCAGTGA 1166
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Db 611 TACTACTACTACTAGAACTACTACTACTACTACTACTAAACTACTACTACTACTACTACTAC 670
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QY 1167 ATGGACAGGAACATCACTA 1186
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Db 671 TACTACCATGACTACTACTA 690
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RESULT 12

FR0048073
 LOCUS Fugu rubripes GSS sequence, clone 263K15bD8, genomic survey
 DEFINITION sequence.
 ACCESSION AL444858
 VERSION AL444858.1 GI:12052694
 KEYWORDS GSS; genome survey sequence.
 SOURCE Takifugu rubripes
 ORGANISM Takifugu rubripes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 Tetraodontidae; Tetraodontidae; Takifugu.
 1 (bases 1 to 494)
 Clark, M.S.
 Direct Submission
 Submitted (29-SEP-2000) MRC Human Genome Mapping Project Resource
 Centre Hinxton, Cambridge, CB10 1SB, UK Email:
 biohelp@hmp.mrc.ac.uk
 Vector: pBluescript II KS
 V type: phagemid
 PRIMER: KS
 DESCR:
 One pass dye-terminator sequencing of BAC (pBelobACII) cloned
 genomic sequence
 The BACs can be obtained from http://www.incyte.com.

REFERENCE
AUTHORS

TITLE Direct Submission
 JOURNAL Submitted (29-SEP-2000) MRC Human Genome Mapping Project Resource
 Centre Hinxton, Cambridge, CB10 1SB, UK Email:
 biohelp@hmp.mrc.ac.uk
 COMMENT Vector: pBluescript II KS
 V type: phagemid
 PRIMER: KS
 DESCR:
 One pass dye-terminator sequencing of BAC (pBelobACII) cloned
 genomic sequence
 The BACs can be obtained from http://www.incyte.com.

FEATURES
source

BASE COUNT 128 a 163 c 45 g 158 t
 ORIGIN
 Query Match 5.8%; Score 71.8; DB 29; Length 494;
 Best Local Similarity 47.1%; Pred. No. 7.9e-07;
 Matches 220; Conservative 0; Mismatches 247; Indels 0; Gaps 0;

QY 755 CTGCTGGTATCGTCCATTTATTGATGCTTATTTCTGTCTACAGATGTTAAACCAATATA 814
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 Db 25 CGGTTTCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTCTGCTG 84
 |||||

QY 815 CTTTACGATATACCAATGATTATATCTTGTCTGCGAGTCGTCGCAAGTAAACCTTTCA 874
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 Db 85 CTACTGCGACGAGCTGCTACTACTACTGCGGCTGCTTCTACTACTGCTACTACTACGA 144
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BASE COUNT	140 a	17 c	140 g	130 t
140 a				
17 c				
140 g				
130 t				

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/clone_lib="WGS-Zmaysp (JM107 adapted methyl filtered)"
/note="Organ: immature ears; Site_1: Xba I; Site_2: Xba I;
The vector was digested with XbaI and one nucleotide was

```

added by fill in in the recessive 3' end. The genomic DNA

was nebulized, end repaired, adaptor ligated and size fractionated using sephadex. The resulting fragments were between 0.8 and 3 kb and were cloned into the vector (x/y reads in M13mp19, b/g reads in pUC19). The same ligation was transformed in either JM107 or DH5a. "

BASE COUNT 112 a 110 c 13 g 115 t
ORIGIN
Query Match 5.6%; Score 69.6; DB 28; Length 350;
Best Local Similarity 52.4%; Pred. No. 2.4e-06;
Matches 153; Conservative 0; Mismatches 139; Indels 0; Gaps 0;
QY 921 TATTGTGATTTGTGTACAACTAGACAGTTACAGACAGTACCTGCTGCTACTACTTT 980
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
6 TACTACTACTTTTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTAC 65
QY 981 ACCATTCAATCCAGTGTGTATTAACCAACCAATCGAAATTTGCCACCTATTCCCAAC 1040
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
66 TAC 125
QY 1041 CACTACCACTCAACATTTCAATGTTGGTGTGACTACTTCTCTATCTGACTAAGACTGCACC 1100
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
126 TACTAGGACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTAC 185
QY 1101 AATTGTGAAACAGCTACTGTTATTGTTGATGTCGACATCATCTACTACCAACACTGTTAC 1160
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
186 TACTACTGCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTAC 245
QY 1161 CAGTGATGGACGAGGACATCATCTACCACTCGTACCAATCCCAACT 1212
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
246 TACTGCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 297

RESULT 15
CNS02HA4 989 bp DNA linear GSS 01-SEP-2000
LOCUS Tetraodon nigroviridis genome survey sequence 17 end of clone
DEFINITION 139021 of library G from Tetraodon nigroviridis, genomic survey
sequence.
AL197365
AL197365.1 GI:7835515
VERSION GSS; genome survey sequence.
KEYWORDS Tetraodon nigroviridis
SOURCE Tetraodon nigroviridis
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Tetraodon.

REFERENCE 1
AUTHORS Roest Crolius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brothier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
TITLE Estimate of human gene number provided by genome-wide analysis
using Tetraodon nigroviridis DNA sequence
JOURNAL Nat. Genet. 25 (2), 235-238 (2000)
MEDLINE 20296633
PUBMED 10835645

REFERENCE 2
AUTHORS Roest Crolius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C.,
Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F.,
Saurin, W., Bernot, A. and Weissenbach, J.
TITLE Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
JOURNAL Genome Res. 10 (7), 939-949 (2000)
MEDLINE 20359837
PUBMED 10899143
REFERENCE 3 (bases 1 to 989)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
PUBMED - Web : www.genoscope.cns.fr

COMMENT This sequence is a single read and was generated as part of a large

scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.

FEATURES
source

1. 989
/organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="139021"
/clone_lib="G"
/note="Genoscope sequence ID : COAG139AH11P1-end : T7"

BASE COUNT 320 a 245 c 122 g 261 t 41 others
ORIGIN

Query Match 5.6%; Score 69.6; DB 29; Length 989;
Best Local Similarity 50.3%; Pred. No. 3.6e-06;
Matches 159; Conservative 4; Mismatches 153; Indels 0; Gaps 0;
QY 911 GATCTAACGGTATTGTTCATTGTTGCTACAACTAGACAGTTTACAGACAGTACCACTGCTG 970
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
4 GATCCATCCTTACCGAGCGCTGCTACTACTACTACTACTACTACTACTACTACTACTACTA 63
QY 971 TCATCTACTTTACCACTTCAATCCAAAGTGTGTATAAAACCAAAACAATCGAAATTTGCAAC 1030
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
64 CTA 123
QY 1031 CTATTCGAACCACTACCACTTCAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1090
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
124 AAACCTACWACWACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTA 183
QY 1091 AGACTGCGACCAATTTGTTGAAACAGCTACTGTTATTGTTGTTGTTGTTGTTGTTGTTG 1150
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
184 CTAATACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTA 243
QY 1151 CAACTGTTTACCACTGAAATGGACAGGAAACAACTACTACCAACCACTGTTGTTGTTGTTGTT 1210
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
244 CTRCTA 303
QY 1211 CTGATTCATTTGACAC 1226
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
304 CTACT 319

Search completed: January 17, 2004, 23:33:50
Job time : 2972 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 17, 2004, 20:47:57 : Search time 89 Seconds
(without alignments)
6174.404 Million cell updates/sec

Title: US-09-715-876-7_COPY_52_1296
Perfect score: 1245
Sequence: 1 aagacaatacactgggtgtttt.....cagtggtgtacaagttcca 1245

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:*

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- 2: /cgm2_6/ptodata/1/ina/5B COMB.seq:*
- 3: /cgm2_6/ptodata/1/ina/6A COMB.seq:*
- 4: /cgm2_6/ptodata/1/ina/6B COMB.seq:*
- 5: /cgm2_6/ptodata/1/ina/PTUS COMB.seq:*
- 6: /cgm2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	82.4	6.6	100	1	US-08-145-705A-32
C 2	82.4	6.6	100	1	US-08-145-705A-34
C 3	76	6.1	100	1	US-08-145-705A-33
C 4	68	5.5	100	1	US-08-145-705A-36
C 5	61.4	4.9	5511	3	US-08-928-361B-2
C 6	61.4	4.9	5511	3	US-09-588-995A-2
C 7	61.4	4.9	7334	3	US-08-928-361B-1
C 8	61.4	4.9	7334	4	US-09-588-995A-1
C 9	57.2	4.6	100	1	US-08-145-705A-37
C 10	57	4.6	100	1	US-08-145-705A-35
C 11	55.2	4.4	5163	3	US-08-700-651-1
C 12	55.2	4.4	5163	3	US-08-928-361B-4
C 13	55.2	4.4	5163	4	US-09-588-995A-4
C 14	55.2	4.4	5318	3	US-08-700-651-2
C 15	55.2	4.4	5318	3	US-08-928-361B-3
C 16	55.2	4.4	5318	4	US-09-588-995A-3
C 17	50	4.0	1071	1	US-08-357-962-1
C 18	50	4.0	1071	1	US-08-878-106-1
C 19	48.6	3.9	425	1	US-08-357-962-5
C 20	48.6	3.9	425	1	US-08-878-106-5
C 21	42.8	3.4	951	4	US-09-328-475C-15
C 22	42.8	3.4	81001	4	US-09-750-580-1
C 23	42.6	3.4	740	3	US-09-451-117-1
C 24	42.6	3.4	740	4	US-09-888-655-1
C 25	42.2	3.4	4249	4	US-09-071-035-403
C 26	42.2	3.4	4359	4	US-09-071-035-401
C 27	41.4	3.3	2349	4	US-09-601-198-46

Sequence 1, Appli
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Sequence 345, App
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Sequence 956, App
Sequence 1254, Ap
Sequence 1555, Ap
Sequence 1, Appli
Sequence 2131, Ap
Sequence 2843, Ap

28 41.2 3.3 6057 3 US-08-362-525-1
29 40.2 3.2 867 4 US-09-216-393B-340
30 40.2 3.2 867 4 US-09-216-393B-342
31 40.2 3.2 1397 4 US-09-216-393B-343
32 40.2 3.2 1397 4 US-09-216-393B-345
33 40 3.2 1023 1 US-08-032-393-1
34 40 3.2 1355 1 US-08-032-393-7
35 39.4 3.2 547 1 US-08-032-393-6
36 39.4 3.2 1664976 4 US-08-916-421B-1
37 38.8 3.1 5340 4 US-09-627-122-21
38 38.4 3.1 1674 4 US-09-134-001C-2732
39 38 3.1 306 4 US-09-328-352-2128
40 37.6 3.0 713 3 US-08-998-416-956
41 37.6 3.0 1614 4 US-09-134-001C-1254
42 37.6 3.0 1674 4 US-09-134-001C-1555
43 37.6 3.0 1664976 4 US-08-916-421B-1
44 37.4 3.0 2187 4 US-09-134-001C-2131
45 37 3.0 888 4 US-09-107-532A-2843

ALIGNMENTS

RESULT 1
US-08-145-705A-32/c
; Sequence 32, Application US/08145705A
; Patent No. 5489513
; GENERAL INFORMATION:
; APPLICANT: Springer, Wolfgang; Plempel, Manfred;
; APPLICANT: L. bberding, Antonius
; TITLE OF INVENTION: SPECIFIC GENE PROBES AND
; TITLE OF INVENTION: PROCESSES FOR THE DIAGNOSTIC
; TITLE OF INVENTION: INVESTIGATION OF CANDIDA
; TITLE OF INVENTION: ALBICANS
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPRUNG HORN KRAMER & WOODS
; STREET: 660 White Plains Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-5144
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.4 MB storage
; COMPUTER: NEC PowerMate 1 Plus
; OPERATING SYSTEM: DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/145,705A
; FILING DATE: October 28, 1993
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: German P 42 36 708.5
; FILING DATE: October 30, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurt G. Briscoe
; REGISTRATION NUMBER: 33,141
; REFERENCE/DOCKET NUMBER: Bayer 8885-KGB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 332-1700
; TELEFAX: (914) 332-1844
; TELEX:
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 100 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Candida albicans

US-08-145-705A-36/c
; Sequence 36, Application US/08145705A
; Patent No. 5489513
; GENERAL INFORMATION:
; APPLICANT: Springer, Wolfgang; Plempel, Manfred;
; APPLICANT: L. Bieding, Antonius
; TITLE OF INVENTION: SPECIFIC GENE PROBES AND
; TITLE OF INVENTION: PROCESSES FOR THE DIAGNOSTIC
; TITLE OF INVENTION: INVESTIGATION OF CANDIDA
; TITLE OF INVENTION: ALBICANS
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPRUNG HORN KRAMER & WOODS
; STREET: 660 White Plains Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-5144
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.4 MB storage
; COMPUTER: NEC PowerMate 1 Plus
; OPERATING SYSTEM: DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/145,705A
; FILING DATE: October 28, 1993
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: German P 42 36 708.5
; FILING DATE: October 30, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurt G. Briscoe
; REGISTRATION NUMBER: 33,141
; REFERENCE/DOCKET NUMBER: Bayer 8885-KGB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 332-1700
; TELEFAX: (914) 332-1844
; TELEX:
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 100 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Candida albicans
; US-08-145-705A-36

Query Match 5.5%; Score 68; DB 1; Length 100;
Best Local Similarity 80.0%; Pred. No. 2.5e-08;
Matches 80; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 719 CATCTAATCGAATTCAGATTAAATATCAAAATCTACTGCTGCTTATCGTCAATTTATG 778
Db 100 CATCTAATGGATCTCTATACATATGAAATATCCCTGAGTTATCGTCAATTTATG 41
QY 779 ATGCTTATATTTCTGTCAGATGTTAAACCAATATATCTT 818
Db 40 ACGTTTATGTAATCTGCTCGGATGTTAAACAGTATATTTT 1

RESULT 5
US-08-928-361B-2
; Sequence 2, Application US/08928361B
; Patent No. 6071518
; GENERAL INFORMATION:
; APPLICANT: Petersen, Carolyn
; TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
; TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
; TITLE OF INVENTION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
; TITLE OF INVENTION: METHODS FOR DETECTION OF CRYPTOSPORIDIUM SPECIES AND

; TITLE OF INVENTION: SPECIES INFECTIONS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PETERS, VERNY, JONES & BIKSA
; STREET: 385 Sherman Avenue, Suite 6
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-1840
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,361B
; FILING DATE: 12-SEP-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,062
; FILING DATE: 13-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verny, Hana
; REGISTRATION/DOCKET NUMBER: 30,518
; REFERENCE/DOCKET NUMBER: 480,76-1(HV)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-1677
; TELEFAX: 650-324-1678
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5511 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-928-361B-2

Query Match 4.9%; Score 61.4; DB 3; Length 5511;
Best Local Similarity 50.9%; Pred. No. 4.2e-06;
Matches 146; Conservative 0; Mismatches 141; Indels 0; Gaps 0;
QY 933 TGCTAACAAGAACAGTTACAGACAGTACCACTGCTGCTACTTACTTACCAATTCATCC 992
Db 1035 TACTACTAGACACACACACACACACACTACTACTACTACTACTACTACTACTACTACTAC 1094
QY 993 AAGTGTTCATATAAACCAAAACAAATCGAAATTTTGCAACTATTCACCACTATCCATCCATC 1052
Db 1095 CACGACAACTACACCAACCACTACCAAGAAACCAACCAACCAACCAACCAACCAAC 1154
QY 1053 AACTTCATATGTTGGTGTGACTACTTCTTCTGACTAGACTGCACCAATTTGGTGAAC 1112
Db 1155 AACTTACTACTACTACACACACACACAACTACTACTACTACTACTACTACTACTACTACT 1214
QY 1113 AGCTACTGTTATTTGTTGATGTGCTATATCATATCACTACTACCACTGTTACCAATGGAAC 1172
Db 1215 TACT 1274
QY 1173 AGGAACAACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 1219
Db 1275 AACCAACAAACAAACAAACAAACAACTACTACTACTACTACTACTACTACTACTACTACT 1321

RESULT 6
US-09-588-995A-2
; Sequence 2, Application US/09588995A
; Patent No. 6514697
; GENERAL INFORMATION:
; APPLICANT: PETERSEN, CAROLYN
; APPLICANT: BARNES, DEBRA A.
; APPLICANT: NELSON, RICHARD C.
; APPLICANT: GUT, JIRI
; TITLE OF INVENTION: METHODS FOR DETECTION OF CRYPTOSPORIDIUM SPECIES AND
; TITLE OF INVENTION: ISOLATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM

```

; TITLE OF INVENTION: INFECTIONS
; FILE REFERENCE: 480.19-5
; CURRENT APPLICATION NUMBER: US/09/588,995A
; CURRENT FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: 08/827,171
; PRIOR FILING DATE: 1997-03-27
; PRIOR APPLICATION NUMBER: 08/928,361
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 08/700,651
; PRIOR FILING DATE: 1996-08-14
; PRIOR APPLICATION NUMBER: 08/415,751
; PRIOR FILING DATE: 1995-04-03
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 5511
; TYPE: DNA
; ORGANISM: Cryptosporidium parvum
; US-09-588-995A-2

Query Match 4.9%; Score 61.4; DB 4; Length 5511;
Best Local Similarity 50.9%; Pred. No. 4.2e-06;
Matches 146; Conservative 0; Mismatches 141; Indels 0; Gaps 0;

Qy 933 TGTACAACTAGAACAGTTACAGACAGTACCACTGCTGTCTACTTTTACCAATTCATCC 992
Db 1035 TACTACTACGACAAACAAACAACTACTACTACTACTACTACTACTACTACTACTACT 1094
Qy 993 AGTGTGTGATAAACCAAAACAACTGCAATTTTCAACCTATTCCACCACTACCAATCC 1052
Db 1095 CACGACAACTACCAACCAACCACTACCAACCAACCAACCAACCAACCAACCAAC 1154
Qy 1053 AACTTCATATGTTGGTGTGACTACTCTCTATCTGACTAAGACTGCACCAATTTGGTGAAC 1112
Db 1155 AACTACTACTACTACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 1214
Qy 1113 AGTACTGTTATTTGATGGCCATATCATATCTACCAACCACTGTTTACCACTGATGGAC 1172
Db 1215 TACTACTACTACTACTACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 1274
Qy 1173 AGGACATATCTACCAACCACTGTTACCAATTCCACTGATTTCAA 1219
Db 1275 AACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 1321

RESULT 7
US-09-588-361B-1
; Sequence 1, Application US/08928361B
; Patent No. 6071518
; GENERAL INFORMATION:
; APPLICANT: Petersen, Carolyn
; TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
; TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS' VARIANTS, ANALOGS AND FRAGMENTS
; TITLE OF INVENTION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
; TITLE OF INVENTION: SPECIES INFECTIONS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PETERS, VERNY, JONES & BIKSA
; STREET: 385 Sherman Avenue, Suite 6
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-1840
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,361B
; FILING DATE: 12-SEP-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/026,062
; FILING DATE: 13-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verny, Hana
; REGISTRATION NUMBER: 30,518
; REFERENCE/DOCKET NUMBER: 480.76-1 (HV)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-1677
; TELEFAX: 650-324-1678
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7334 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-928-361B-1

Query Match 4.9%; Score 61.4; DB 3; Length 7334;
Best Local Similarity 50.9%; Pred. No. 4.6e-06;
Matches 146; Conservative 0; Mismatches 141; Indels 0; Gaps 0;

Qy 933 TGTACAACTAGAACAGTTACAGACAGTACCACTGCTGTCTACTTTTACCAATTCATCC 992
Db 2703 TACTACTACGACAAACAAACAACTACTACTACTACTACTACTACTACTACTACTACT 2762
Qy 993 AGTGTGTGATAAACCAAAACAAATCGAAATTTTGGCAACTTATTCACCACTACCAATCC 1052
Db 2763 CACGACAACTACCAACCAACCACTACCAACCAACCAACCAACCAACCAACCAACCAAC 2822
Qy 1053 AACTTCATATGTTGGTGTGACTACTTCTATCTGACTAAGACTGCACCAATTTGGTGAAC 1112
Db 2823 AACTACTACTACTACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 2882
Qy 1113 AGTACTGTTATTTGATGGCCATATCATATCTACCAACCACTGTTTACCACTGATGGAC 1172
Db 2883 TACTACTACTACTACTACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 2942
Qy 1173 AGGACATATCTACCAACCACTGTTACCAATTCCACTGATTTCAA 1219
Db 2943 AACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 2989

RESULT 8
US-09-588-995A-1
; Sequence 1, Application US/09588995A
; Patent No. 6514697
; GENERAL INFORMATION:
; APPLICANT: PETERSEN, CAROLYN
; APPLICANT: BARNES, DEBRA A.
; APPLICANT: NELSON, RICHARD C.
; APPLICANT: GUT, JIRI
; TITLE OF INVENTION: METHODS FOR DETECTION OF CRYPTOSPORIDIUM SPECIES AND
; TITLE OF INVENTION: ISOLATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM
; TITLE OF INVENTION: INFECTIONS
; FILE REFERENCE: 480.19-5
; CURRENT APPLICATION NUMBER: US/09/588,995A
; CURRENT FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: 08/827,171
; PRIOR FILING DATE: 1997-03-27
; PRIOR APPLICATION NUMBER: 08/928,361
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 08/700,651
; PRIOR FILING DATE: 1996-08-14
; PRIOR APPLICATION NUMBER: 08/415,751
; PRIOR FILING DATE: 1995-04-03
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 7334
; TYPE: DNA
; ORGANISM: Cryptosporidium parvum
; US-09-588-995A-1
```

Query Match	4.9%;	Score 61.4;	DB 4;	Length 7334;
Best Local Similarity	50.9%;	Pred. No. 4.6e-06;		
Matches 146;	Conservative 0;	Mismatches 141;	Indels 0;	Gaps 0;
Qy	933	TGCTACAACTAGAAACAGTTACAGACAGTACCACTGCTGTGCTCACTACTTCTTTACCAATTCATCC	992	
Db	2703	TACTTACTACGACAAACAACAACAACTACTTACTTACTTACAGCCAACTACTACAAC	2762	
Qy	993	AAGTGTGTGATTAACCAACCAACAACTCGAAATTTTGCACCACTATTTCCACCACTACCATCAC	1052	
Db	2763	CACGCAAACTACCAACCAACCAACCACTCCAGAAACCAACAACAACAACAACAAC	2822	
Qy	1053	AACTTCATATGTTGGTGTGACTACTTCCCTATCTGACTAAGACGTGCACAAATTGGTGAAC	1112	
Db	2823	AACTTACTTACTACCAACAACAACAACAACCTACTTACTTACTTACTTACTTACTTACT	2882	
Qy	1113	AGCTACTGTTATTGTTGATGTGCCATATCATCTTACCACAACCTGTTTACCAGTCAATGGAC	1172	
Db	2883	TACTTACTTACTTACTTACTACCAACAACCAACAACCAACCAACTTACCAGAAACCAAC	2942	
Qy	1173	AGGAACAATCACTACCAACCAACTCGTACCAATCCAACTGATTCAA	1219	
Db	2943	AACAACAACAACAACAACAACAACCTTACTTACTTACCAACCAACCAAA	2989	

RESULT 9
 US-08-145-705A-37/c
 ; Sequence 37, Application US/08145705A
 ; Patent No. 5489513
 ;
 ; GENERAL INFORMATION:
 ; APPLICANT: Springer, Wolfgang; Plempel, Manfred;
 ; APPLICANT: L bberding, Antonius
 ; TITLE OF INVENTION: SPECIFIC GENE PROBES AND
 ; TITLE OF INVENTION: PROCESSES FOR THE DIAGNOSTIC
 ; TITLE OF INVENTION: INVESTIGATION OF CANDIDA
 ; TITLE OF INVENTION: ALBICANS
 ; NUMBER OF SEQUENCES: 44
 ;
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: SPRUNG HORN KRAMER & WOODS
 ; STREET: 660 White Plains Road
 ; CITY: Tarrytown
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10591-5144
 ;
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.5 inch, 1.4 MB storage
 ; COMPUTER: NEC PowerMate 1 Plus
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: WordPerfect 5.1
 ;
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/145,705A
 ; FILING DATE: October 28, 1993
 ; CLASSIFICATION: 536
 ;
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: German P 42 36 708.5
 ; FILING DATE: October 30, 1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kurt G. Briscoe
 ; REGISTRATION NUMBER: 33,141
 ; REFERENCE/DOCKET NUMBER: Bayer 8885-KGB
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (914) 332-1700
 ; TELEFAX: (914) 332-1844
 ; TELEX:
 ;
 ; INFORMATION FOR SEQ ID NO: 37:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 100 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHETICAL: NO

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; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Candida albicans
US-08-145-705A-37

Query Match      4.6%  Score 57.2; DB 1; Length 100;
Best Local Similarity 80.6%; Pred.No. 1.3e-05;
Matches 79; Conservative 0; Mismatches 18; Indels

Qy 620 CTATTGATGCTCAAATATTTCATATTGGTATCAAAAAGGAGTAAATGATT
Db 98 CTATAGACTGTTCAAATGTTTCATATTGGGATTTTCAAAGGAGTGAATGATT
Qy 680 CGGTTTCACCTGAATCATTTAGTTACACTAAAACCTGTT 717
Db 39 CGTTATCATATGATTCATTTAGTTTACAGAAAATGTT 2

RESULT 10
US-08-145-705A-35/c
; Sequence 35, Application US/08145705A
; Patent No. 5489513
; GENERAL INFORMATION:
; APPLICANT: Springer, Wolfgang; Plempel, Manfred;
; APPLICANT: L bberding, Antonius
; TITLE OF INVENTION: SPECIFIC GENE PROBES AND
; TITLE OF INVENTION: PROCESSES FOR THE DIAGNOSTIC
; TITLE OF INVENTION: INVESTIGATION OF CANDIDA
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESS: SPRUNG HORN KRAMER & WOODS
; STREET: 660 White Plains Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-5144
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.4 MB storage
; COMPUTER: NEC PowerMate 1 Plus
; OPERATING SYSTEM: DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/145,705A
; FILING DATE: October 28, 1993
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: German P 42 36 708.5
; FILING DATE: October 30, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurt G. Briscoe
; REGISTRATION NUMBER: 33,141
; REFERENCE/DOCKET NUMBER: Bayer 8895-KGB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 332-1700
; TELEFAX: (914) 332-1844
; TELEX:
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 100 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Candida albicans
US-08-145-705A-35

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Query Match 4.6%; Score 57; DB 1; Length 100;
Best Local Similarity 74.2%; Pred. No. 1.5e-05;
Matches 72; Conservative 0; Mismatches 25; Indels


```

; LENGTH: 5318 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-928-361B-3

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Query Match	4.4%;	Score 55.2;	DB 3;	Length 5318;	
Best Local Similarity	48.4%;	Pred. No. 0.00015;			
Matches. 153;	Conservative 0;	Mismatches 163;	Indels 0;	Gaps 0;	
QY	912	ATCTACGGTATTGTTCATTTGGTCTCAACTAGACAGATTGTACAGACAGTACCACTGCTGT	971		
DB	591	AAC TACTTACTTACTTACTACGCAACACACACACACACGACACACACACTACTACTAC	650		
QY	972	CAC TACTTTTACCAATTCATTCCTCAAGTTGTGATAAAACCAAAACAAATCGAAATTTTGCAACC	1031		
DB	651	AACTACTTACCCTACTACTACGCAACACCAACCAACCAACCAACCAACCAACCAAC	710		
QY	1032	TATTCCAAACCACTACCATCACAACCTTCATATGTTGGTGGACACTTCTCTACTCTGACTAA	1091		
DB	711	AACAACCAACCAACCAACCAACCAACGACTACTACTACTACTACTACTACTACTACTACT	770		
QY	1092	GACTGCACCAATTTGGTGAACACGACTCTGTTATTTGATGTGCGCATATCATACTACTACC	1151		
DB	771	TACTTACTACCAACCAACCAACCAACTAACCCAACTACACCAACCACTACACCAAC	830		
QY	1152	AACTGTTTACCAGTGAATGGA CAGGAACAAATCACTTACCACCAACAACTGGTACCAATCCAAC	1211		
DB	831	AACAACCAACCAACCAACCACTACCAACCACTCAACCCACCAACCAACCACTACAACCAACCAAC	890		
QY	1212	TGATTCAATTTGACACA	1227		
DB	891	CACAACCAACCAACCAACA	906		

Search completed: January 17, 2004, 22:44:09
Job time : 91 secs

QY 1019 AAAAAAAAACTATTCCAACTACCACTACCACTCATCATCTCATCTGTTGGTGCATCTT 1078
 |||||
 Db 100 AAAAAAAAACTATTCCAACTACCACTACCACTCATCATCTCATCTGTTGGTGCATCTT 41
 |||||

QY 1079 CTTATCTGACTAGACTGACCACTGTTGGTGAACAGCTAC 1118
 |||||
 Db 40 CCTACAGAACCAAACTGTACCAATAGGACAACTGCTAC 1
 |||||

RESULT 4
 AAQ62592/c
 ID AAQ62592 standard; DNA; 100 BP.
 XX
 AC AAQ62592;
 XX
 DT 25-MAR-2003 (updated)
 DT 07-DEC-1994 (first entry)
 XX
 XX
 DE Candida albicans-specific hybridisation probe.
 XX
 KW DNA hybridisation probe; detection; assay; C. albicans yeast;
 KW species specific sequence; ss.
 XX
 OS Candida albicans.
 XX
 PN EP595167-A1.
 XX
 PD 04-MAY-1994.
 XX
 PF 19-OCT-1993; 93BP-0116865.
 XX
 PR 30-OCT-1992; 92DE-4236708.
 XX
 XX (FARB) BAYER AG.
 XX
 XX Loebberding A, Flempel M, Springer W;
 PI WPI; 1994-145805/18.
 DR
 XX

PT New hybridisation reagents specific for Candida albicans - are
 PT polynucleotide and oligo-nucleotide probes, providing high
 PT sensitivity and early diagnosis of infection
 PS Claim 9; Page 34; 44pp; German.
 XX
 CC A C. albicans gene library was prepared in pBR322 and inserts were
 CC selected for multiple presence in the genome, strong conservation
 CC without deletions or insertions and absolute specificity for
 CC C. albicans. Gene probe 431.19 (AAQ62552) hybridised to all but 4 of
 CC the 87 clinical isolates of C. albicans being tested. A clone (436.1)
 CC was then isolated from the 4 isolates not recognised by 431.19. Some
 CC 10mer oligonucleotides covering the complete sequences of 431.19
 CC and 436.1 were synthesised and tested (see AAQ62558-Q62594). All were
 CC found to be absolutely specific for C. albicans.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 100 BP; 39 A; 15 C; 19 G; 27 T; 0 other;

Query Match 5.5%; Score 68; DB 15; Length 100;
 Best Local Similarity 80.0%; Pred. No. 1.5e-06;
 Matches 80; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 719 CATCTAATGGATTCAGATTAATATCAATGATCACTGCTGTTATGTCCTCATTTATG 778
 |||||
 Db 100 CATCTAATGGATTCCTCTCATCATATGAAATATCCCTGCAGGTATGCTCATTTATG 41
 |||||
 QY 779 ATGCTTATTTCTGTACAGATGTTAACTAATATCTTT 818
 |||||
 Db 40 ACGTTTATGTTATCTGCTCCGGATGTTAAACAGTATATTT 1
 |||||

RESULT 5
 AAA61847

ID
 XX
 AC AAA61847 standard; DNA; 5511 BP.
 XX
 DT 28-OCT-2000 (first entry)
 XX
 DE Cryptosporidium parvum Iowa isolate GP900 ORP.
 XX
 KW GP900; Iowa isolate; glycoprotein; antibody; cryptosporidiosis;
 KW competitive inhibition; attachment; invasion; ligand binding; sporozoite;
 KW merozoite; diarrhoea; protozoa; open reading frame; ORF; ds.
 XX
 OS Cryptosporidium parvum.
 XX
 FH Key Location/Qualifiers
 CDS 1.5511
 FT /*tag= a
 FT /product= "Cryptosporidium parvum Iowa isolate GP900"
 FT /note= "No stop codon given"
 XX
 PN US6071518-A.
 XX
 PD 06-JUN-2000.
 XX
 PF 12-SEP-1997; 97US-0928361.
 XX
 PR 13-SEP-1996; 96US-0026062.
 PR 01-JUN-1993; 93US-0071880.
 PR 29-MAY-1992; 92US-0891301.
 PR 03-APR-1995; 95US-0415751.
 PR 14-AUG-1996; 96US-0700651.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Petersen C;
 XX
 DR WPI; 2000-422065/36.
 DR P-PSDB; AAB11726.
 XX

PT New GP900 protein fragments and fusion proteins of Cryptosporidium
 PT parvum, useful for detecting the presence of the parasite, and
 PT diagnosing or treating Cryptosporidium infections by competitive
 PT inhibition of the function of GP900 -
 XX
 PS Claim 16; Column 37-42; 59pp; English.
 XX
 CC The invention relates to the GP900 glycoprotein of the protozoan
 CC Cryptosporidium parvum. DNA encoding it, GP900 fragments, and fusion
 CC proteins comprising GP900 fragments. The invention also relates to the
 CC administration of GP900 or fragments thereof to a host to elicit anti-
 CC GP900 antibody production, and to a method of cryptosporidiosis treatment
 CC or prophylaxis comprising administration of anti-GP900 antibodies to an
 CC individual. Cryptosporidium parvum GP900 and GP900 fragments are able to
 CC competitively inhibit sporozoite or merozoite attachment or invasion, and
 CC are also useful for the generation of anti-GP900 antibodies. The
 CC antibodies also inhibit sporozoite or merozoite attachment/invasion and
 CC additionally inhibit the binding of GP900 ligands to GP900. GP900
 CC prevent cryptosporidiosis. Infection with Cryptosporidium is a common
 CC cause of diarrhoea in humans and causes life-threatening diarrhoea in
 CC immunocompromised persons. Cryptosporidiosis can be contracted from
 CC contaminated municipal water supplies (e.g., public swimming pools). It
 CC is also a cause of disease in animals, resulting in financial losses in
 CC agriculture. GP900 fragments, fusion proteins and antibodies may also be
 CC used for the diagnosis of Cryptosporidium parvum infections, and for the
 CC detection of the parasite in the environment. The present sequence
 CC represents the open erasing frame (ORF) encoding the GP900 protein of the
 CC Iowa isolate of Cryptosporidium parvum.
 XX
 SQ Sequence 5511 BP; 1964 A; 1204 C; 944 G; 1399 T; 0 other;

Query Match 4.9%; Score 61.4; DB 21; Length 5511;
 Best Local Similarity 50.9%; Pred. No. 0.00014;

PS Claim 16; Column 31-38; 59pp; English.

XX The invention relates to the GP900 glycoprotein of the protozoan
CC Cryptosporidium parvum, DNA encoding it, GP900 fragments, and fusion
CC proteins comprising GP900 fragments. The invention also relates to the
CC administration of GP900 or fragments thereof to a host to elicit anti-
CC GP900 antibody production, and to a method of cryptosporidiosis treatment
CC or prophylaxis comprising administration of anti-GP900 antibodies to an
CC individual. Cryptosporidium parvum GP900 and GP900 fragments are able to
CC competitively inhibit sporozoite or merozoite attachment or invasion, and
CC are also useful for the generation of anti-GP900 antibodies. The
CC antibodies also inhibit sporozoite or merozoite attachment/invasion and
CC additionally inhibit the binding of GP900 ligands to GP900. GP900
CC proteins, fragments and antibodies may therefore be used to treat or
CC prevent cryptosporidiosis. Infection with Cryptosporidium is a common
CC cause of diarrhoea in humans and causes life-threatening diarrhoea in
CC immunocompromised persons. Cryptosporidiosis can be contracted from
CC contaminated municipal water supplies (e.g., public swimming pools). It
CC is also a cause of disease in animals, resulting in financial losses in
CC agriculture. GP900 fragments, fusion proteins and antibodies may also be
CC used for the diagnosis of Cryptosporidium parvum infections, and for the
CC detection of the parasite in the environment. The present sequence
CC represents genomic DNA encoding the GP900 protein of the Iowa isolate of
CC Cryptosporidium parvum.

SQ Sequence 7334 BP; 2629 A; 1536 C; 1261 G; 1908 T; 0 other;

Query Match 4.9%; Score 61.4; DB 21; Length 7334;
Best Local Similarity 50.9%; Pred. No. 0.00015;
Matches 146; Conservative 0; Mismatches 141; Indels 0; Gaps 0;

QY 933 TGTCTACAACTAGAACAGTTACAGACAGTACAGACAGTGTGTCACCTTTTACCATTCAATCC 992
DB 2703 TACTACTACGACACACAACTACTACTACTACTACTACTACTACTACTACTACTACTAC 2762

QY 993 AAGTGTGTGATAAACAACCAACAACTCGAAATTTTGCACCTATTTCCAACTACTACCATCAC 1052
DB 2763 CAGGACAACTACACCAACCACTACCAAGAACCAACCAACCAACCAACCAAC 2822

QY 1053 AACTTCATATGTTGGTGTGACTACTTCTTATCTGACTAAGACTGCACCAATTTGGTGAAC 1112
DB 2823 AACTTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTAC 2882

QY 1113 AGTACTGTTATGTTGATGTGCGCATATCATCTACTACCAACTGTTTACCAGTGAATGGAC 1172
DB 2883 TAC 2942

QY 1173 AGGAACAATCACTTACCACCACTCGTACCAATCCAACTGATTCAA 1219
DB 2943 AACAAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACA 2989

RESULT 8
ABT04775
ID ABT04775 standard; DNA; 7334 BP.
XX AC ABT04775;
XX
DT 27-SEP-2002 (first entry)
DE C parvum GP900 gene fragment SEQ ID NO: 1.
XX
XX Cryptosporidium detection; GP900; P68; cryptopain; cryptosporidiosis;
KW gene; db.
XX Cryptosporidium parvum.
OS WO200194631-A1.
PN
XX 13-DEC-2001.
XX
XX 14-MAY-2001; 2001WO-US15624.

PR 06-JUN-2000; 2000US-0588995.

XX (REGC) UNIV CALIFORNIA.

XX Petersen C, Barnes DA, Nelson RG, Gut J;

XX WPI; 2002-566447/60.

XX Detecting Cryptosporidium in biological and environmental samples and
PT diagnosis of cryptosporidiosis involves, contacting the sample with
PT Cryptosporidium GP900, P68 or cryptopain antigen, antibody, DNA or RNA

XX Disclosure; Page 97-99; 157pp; English.

XX The present invention relates to a method of detecting Cryptosporidium in
CC biological and environmental samples, and of diagnosing
CC cryptosporidiosis. This involves obtaining a sample and contacting it
CC with Cryptosporidium GP900, P68 or cryptopain antigen, antibody, DNA or
CC RNA, or its variant, mutant or fragment. The method is also useful for
CC detecting and identifying individual Cryptosporidium isolates based on
CC the genetic characteristics, and for diagnosis of prior or concurrent
CC Cryptosporidium infection. The present sequence is a C. parvum coding
CC sequence used in the exemplification of the invention.

SQ Sequence 7334 BP; 2627 A; 1536 C; 1263 G; 1908 T; 0 other;

Query Match 4.9%; Score 61.4; DB 24; Length 7334;
Best Local Similarity 50.9%; Pred. No. 0.00015;
Matches 146; Conservative 0; Mismatches 141; Indels 0; Gaps 0;

QY 933 TGTCTACAACTAGAACAGTTACAGACAGTGTGTCACCTTTTACCATTCAATCC 992
DB 2703 TACTACTACGACACACAACTACTACTACTACTACTACTACTACTACTACTACTACTAC 2762

QY 993 AAGTGTGTGATAAACAACCAACAACTCGAAATTTTGCACCTATTTCCAACTACTACCATCAC 1052
DB 2763 CAGGACAACTACACCAACCACTACCAAGAACCAACCAACCAACCAACCAAC 2822

QY 1053 AACTTCATATGTTGGTGTGACTACTTCTTATCTGACTAAGACTGCACCAATTTGGTGAAC 1112
DB 2823 AACTTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTAC 2882

QY 1113 AGTACTGTTATGTTGATGTGCGCATATCATCTACTACCAACTGTTTACCAGTGAATGGAC 1172
DB 2883 TAC 2942

QY 1173 AGGAACAATCACTTACCACCACTCGTACCAATCCAACTGATTCAA 1219
DB 2943 AACAAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACA 2989

RESULT 9
AAQ62593/c
ID AAQ62593 standard; DNA; 100 BP.
XX AC AAQ62593;
XX
DT 25-MAR-2003 (updated)
DT 07-DEC-1994 (first entry)
DE Candida albicans-specific hybridisation probe.
XX DNA hybridisation probe; detection; assay; C. albicans yeast;
KW species specific sequence; ss.
XX Candida albicans.
XX EP595167-A1.
XX
XX 04-MAY-1994.
XX
XX 19-OCT-1993; 93EP-0116865.

CC from human breast and BT 474 cells. The method involves contacting
CC the probes with a collection of detectably labelled nucleic acids
CC derived from mRNA of human breast, and then measuring the label
CC bound to each probe of the microarray. The probes are useful for
CC verifying the expression of regions of genomic DNA predicted to
CC encode proteins. They are useful for gene discovery, and for
CC determining predisposition and/or prognosing breast disease. Gene
CC expression analysis is useful for assessing the toxicity of chemical
CC agents on cells. The microarray of this invention presents a far greater
CC diversity of probes for measuring gene expression, with far less bias
CC than expressed sequence tag microarrays. The method is suitable for
CC rapid production of functional information from genomic sequence. The
CC present sequence is a single exon nucleic acid probe of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 436 BP; 137 A; 144 C; 15 G; 140 T; 0 other;

Query Match 4.4%; Score 55.4; DB 22; Length 436;
Best Local Similarity 48.6%; Pred. No. 0.0019;
Matches 152; Conservative 0; Mismatches 161; Indels 0; Gaps 0;
QY 914 CTAACGGTATTGTCATTTGCTACAACTAGAACAGTTACAGACAGTACCTGCTGCA 973
DB 68 CTATTGTCACTACTATTACCACTACATTTAGTACTACCACTATCATCTACATCA 127
QY 974 CTACTTTTACCAATTCATCCAGTGTGTATATAACCAAAACATCGAAATTTGCAACCTA 1033
DB 128 CTACTTAATCTACTATTACCACTACTATTACCACTATACCACTATCATCTACTA 187
QY 1034 TTCGAACACACTACATCACTCATTTGTTGGTGTGACTACTTCTCTATCTGACTAGA 1093
DB 188 CCACCTCCCACTACTACTATTAATGCTATCATCTACTACTGCTCTATTAATTA 247
QY 1094 CTGACCAAAATGGTGAACAGTACTGTTATTGTTGATGTCATATCATCTACCA 1153
DB 248 CTCTACTCTCCATTTACTACTACTAGTAGTATACCACTACTACTACTACTATCA 307
QY 1154 CTGTTACAGTGAATGGACAGGAACATCACTACCAACCACTCGTACCAATCCA 1213
DB 308 CTATTACCAACCACTACTACTATCATCTACTACTACTACTACCACTACTACTG 367
QY 1214 ATTCAATTGACAC 1226
DB 368 CTGTCATTACTAC 380

RESULT 12
ABA54635
ID ABA54635 standard; DNA; 436 BP.
XX ABA54635;
AC ABA54635;
XX
DT 01-FEB-2002 (first entry)
XX Human foetal liver single exon nucleic acid probe #2940.
DE Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
XX Homo sapiens.
XX WO200157277-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US00669.
XX
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483447/52.
XX Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human fetal liver -
PT
XX
XX Claim 1; SEQ ID NO 2940; 639pp + sequence listing; English.
XX
XX The invention relates to a single exon nucleic acid probe for
XX measuring human gene expression in a sample derived from human foetal
XX liver. The single exon nucleic acid probes may be used for predicting,
XX measuring and displaying gene expression in samples derived from human
XX foetal liver. The present sequence is a single exon nucleic acid
XX probe of the invention.
XX Note: The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 436 BP; 137 A; 144 C; 15 G; 140 T; 0 other;

Query Match 4.4%; Score 55.4; DB 22; Length 436;
Best Local Similarity 48.6%; Pred. No. 0.0019;
Matches 152; Conservative 0; Mismatches 161; Indels 0; Gaps 0;
QY 914 CTAACGGTATTGTCATTTGCTACAACTAGAACAGTTACAGACAGTACCTGCTGCA 973
DB 68 CTATTGTCACTACTATTACCACTACATTTAGTACTACCACTATCATCTACATCA 127
QY 974 CTACTTTTACCAATTCATCCAGTGTGTATATAACCAAAACATCGAAATTTGCAACCTA 1033
DB 128 CTACTTAATCTACTATTACCACTACTATTACCACTATCATCTACTACTA 187
QY 1034 TTCGAACACACTACATCACTCATTTGTTGGTGTGACTACTTCTCTATCTGACTAGA 1093
DB 188 CCACCTCCCACTACTACTATTAATGCTATCATCTACTACTACTACTATCA 247
QY 1094 CTGACCAAAATGGTGAACAGTACTGTTATTGTTGATGTCATATCATCTACCA 1153
DB 248 CTCTACTCTCCATTTACTACTACTAGTAGTATACCACTACTACTACTACTATCA 307
QY 1154 CTGTTACAGTGAATGGACAGGAACATCACTACCAACCACTCGTACCAATCCA 1213
DB 308 CTATTACCAACCACTACTACTATCATCTACTACTACTACTACCACTACTACTG 367
QY 1214 ATTCAATTGACAC 1226
DB 368 CTGTCATTACTAC 380

RESULT 13
ABA24419
ID ABA24419 standard; DNA; 436 BP.
XX ABA24419;
AC ABA24419;
XX
DT 23-JAN-2002 (first entry)
XX Probe #2885 for gene expression analysis in human heart cell sample.
XX Human; gene expression; heart; microarray; vascular system; probe;
XX cardiovascular disease; hypertension; cardiac arrhythmia;
XX congenital heart disease; ss.
XX Homo sapiens.
XX OS
XX 2000US-0234687.
XX
XX 2000US-0234687.

PD 09-AUG-2001.
XX 30-JAN-2001; 2001WO-US00666.
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0623266.
XX 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488899/53.
XX Single exon nucleic acid probes for analyzing gene expression in human
XX hearts -
XX Claim 1; SEQ ID No 2885; 530pp; English.
XX The present invention relates to single exon nucleic acid probes for
XX measuring human gene expression in a sample derived from human heart. The
XX present sequence is one such probe. The probes may be used for
XX predicting, measuring and displaying gene expression in samples derived
XX from the human heart via microarrays. By measuring gene expression, the
XX probes are useful for predicting, diagnosing, grading, staging,
XX monitoring and prognosing diseases of the human heart and vascular system
XX e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
XX congenital heart disease.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 436 BP; 137 A; 144 C; 15 G; 140 T; 0 other;
Query Match 4.4%; Score 55.4; DB 22; Length 436;
Best Local Similarity 48.6%; Pred. No. 0.0019;
Matches 152; Conservative 0; Mismatches 161; Indels 0; Gaps 0;
QY 914 CTACGGTATGTCATGTTGCTACCACTAGAACAGTTACAGACAGTACCTGCTGTCA 973
DB 68 CTATTGTCATCTATTACCACTTACCATTAGTACTACCACTACCTATCATCTACCATCA 127
QY 974 CTACTTTACCATTCATCCAGTGTGATATAAACCAAAACAAATCGAAATTTTGCACCTA 1033
DB 128 CTACTTAATCTATCATCTACCTACTATTAATCCATTAACCACTATCATCTACTACTA 187
QY 1034 TTCCAAACCACTACCATCACTTCAATGTTGATGTTGCTGCTACTTCTTCTGACTTAAGA 1093
DB 188 CCACCTCCACCACTTACTACTACTATTAATGCTATCACTACTGCTTCTATAATTACTA 247
QY 1094 CTGACCAATGTTGTAACAGCTACTGTTATGTTGCTGCTACTTCTTCTGACTTAAGA 1153
DB 248 CTGCTACTCTCCACCACTTACTACTATTAATGCTATCACTACTGCTTCTATAATTACTA 307
QY 1154 CTGTTACCACTGTAATGGAACAGCTACTGTTATGTTGCTGCTACTTCTTCTGACTTAAGA 1213
DB 308 CTATTACCACTCCACCACTTACTACTATTAATGCTATCACTACTGCTTCTATAATTACTA 367
QY 1214 ATTCAATTGACAC 1226
DB 368 CTGTCATTACTAC 380.
RESULT 14
ID AAK02925
XX AAK02925 standard; DNA; 436 BP.
XX AAK02925;
XX

DT 05-NOV-2001 (first entry)
XX Human brain expressed single exon probe SEQ ID NO: 2916.
DE
XX
KW Human; brain expressed exon; gene expression analysis; probe;
KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
KW epilepsy; cancer; ss.
OS Homo. sapiens.
FN WO200157275-A2.
XX
PD 09-AUG-2001.
XX 30-JAN-2001; 2001WO-US00667.
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0623266.
XX 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483446/52.
XX Single exon nucleic acid probes for analyzing gene expression in human
XX brains -
XX Example 4; SEQ ID NO: 2916; 650pp + Sequence Listing; English.
XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX brain. They can be used to measure gene expression in brain cell samples,
XX which may enable the diagnosis and improved treatment of nervous system
XX diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX epilepsy and cancers. The present sequence is one of the probes of the
XX invention.
XX Sequence 436 BP; 137 A; 144 C; 15 G; 140 T; 0 other;
Query Match 4.4%; Score 55.4; DB 22; Length 436;
Best Local Similarity 48.6%; Pred. No. 0.0019;
Matches 152; Conservative 0; Mismatches 161; Indels 0; Gaps 0;
QY 914 CTACGGTATGTCATGTTGCTACCACTAGAACAGTTACAGACAGTACCTGCTGTCA 973
DB 68 CTATTGTCATCTATTACCACTTACCATTAGTACTACCACTATCATCTACTACTACATCA 127
QY 974 CTACTTTACCATTCATCCAGTGTGATATAAACCAAAACAAATCGAAATTTTGCACCTA 1033
DB 128 CTACTTAATCTATCATCTACCTACTATTAATCCATTAACCACTATCATCTACTACTA 187
QY 1034 TTCCAAACCACTACCATCACTTCAATGTTGATGTTGCTGCTACTTCTTCTGACTTAAGA 1093
DB 188 CCACCTCCACCACTTACTACTATTAATGCTATCACTACTGCTTCTATAATTACTA 247
QY 1094 CTGACCAATGTTGTAACAGCTACTGTTATGTTGCTGCTACTTCTTCTGACTTAAGA 1153
DB 248 CTGCTACTCTCCACCACTTACTACTATTAATGCTATCACTACTGCTTCTATAATTACTA 307
QY 1154 CTGTTACCACTGTAATGGAACAGCTACTGTTATGTTGCTGCTACTTCTTCTGACTTAAGA 1213
DB 308 CTATTACCACTCCACCACTTACTACTATTAATGCTATCACTACTGCTTCTATAATTACTA 367
QY 1214 ATTCAATTGACAC 1226
DB 368 CTGTCATTACTAC 380

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RESULT 15
AAK28369
ID AAK28369 standard; DNA; 436 BP.
XX
AC AAK28369;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human bone marrow expressed single exon probe SEQ ID NO: 2926.
XX
KW Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX
OS Homo sapiens.
XX
FN WO200157276-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00668.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488900/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human bone marrow -
XX
PS Example 4; SEQ ID NO: 2926; 658pp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in bone marrow
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukaemia and myeloma. The present sequence is one of
CC the probes of the invention.
XX
SQ Sequence 436 BP; 137 A; 144 C; 15 G; 140 T; 0 other;

Query Match 4.4%; Score 55.4; DB 22; Length 436;
Best Local Similarity 48.6%; Pred. No. 0.0019;
Matches 152; Conservative 0; Mismatches 161; Indels 0; Gaps 0;

QY 914 CTAACGGTATTGTCATTGTTGTACAACTAGAACAGTTACAGACAGTACCACTGCTGTCA 973
DB 68 CTAATGTCACCTACTATTACCACTACCACTATGATGATGATGATGATGATGATGATGAT 127
QY 974 CTACTTTTACCATTCAATCCAGTGTGATATAAACCAGAACAAATCGAAATTTTGCAACCTA 1033
DB 128 CTACTAATCTATCATTTACCACTACTATTTACCACTATTTACCACTATTTACCACTACTA 187
QY 1034 TTCCAAACCACTACCACTACCACTTCCATATGTTGGTGTGACTATTTCTATCTGACTAAGA 1093
DB 188 CCACCTCCACCACTACTACTACTAATGCTATCATTTACTACTACTACTACTACTACTACTA 247
QY 1094 CTGCACCAATTTGGTGAACAGTACTGTTATTTGTTGATGTTGCTATCTACTACTACCAAA 1153
DB 248 CTCCTACTCCCTACCACTACTACTACTAGTAGTATCACCATTACTACTACTACTACTACTAT 307
QY 1154 CTGTTACCACTGAATGGACAGGAAACAATCACTACCACTACCACTACCACTACCACTG 1213
DB 308 CTATTACCACCACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTCTG 367
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QY 1214 ATTCAATTGACAC 1226
DB 368 CTGTCATTACTAC 380
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Search completed: January 17, 2004, 21:22:32
Job time : 384 secs

52 to 1296 of SEQ ID NO.7

RESULT 1
YSAALS1
LOCUS YSAALS1 3786 bp DNA linear PLN 03-MAY-2000
DEFINITION Candida albicans agglutinin-like sequence (ALS1) gene, complete
cde.
ACCESSION L25902
VERSION L25902.1 GI:704426
KEYWORDS
SOURCE Candida albicans
ORGANISM Candida albicans
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
REFERENCE 1 (bases 1 to 3786)
AUTHORS Hoyer,L.L., Scherer,S., Shatzman,A.R. and Livi,G.P.
TITLE Candida albicans ALS1: domains related to a Saccharomyces

to have a

